

| OM protein - protein search, using sw model | | | | | | |
|--|---|-------------|--------|---|-------------------|-------------------|
| Run on: | May 6, 2005, 17:11:07 ; Search time 16.8027 Seconds | | | (without alignment) | | |
| Title: | US-10-072-159-11 | | | 577.548 Million cell updates/sec | | |
| Perfect score: | 708 | | | 1 FSVGLELIVYTINPPNPIRFTK. YADNDNDSTFGFLYHDIN 130 | | |
| Scoring table: | BLOSUM62 | | | Gapop 10.0 , Gapext 0.5 | | |
| Searcher: | 513545 seqs, 74649064 residues | | | | | |
| Total number of hits satisfying chosen parameters: | 513545 | | | | | |
| Minimum DB seq length: | 0 | | | | | |
| Maximum DB seq length: | 200000000 | | | | | |
| Post-processing: | Minimum Match 0% | | | | | |
| | Maximum Match 100% | | | | | |
| Database : | Issued Patents AA;* | | | | | |
| Result No. | Score | Query Match | Length | DB ID | Description | |
| 1 | 708 | 100.0 | 130 | 3 | US-09-485-316A-11 | Sequence 11, Appi |
| 2 | 708 | 100.0 | 231 | 4 | US-09-485-316A-11 | Sequence 2, Appi |
| 3 | 708 | 100.0 | 244 | 2 | US-08-463-911-7 | Sequence 7, Appi |
| 4 | 708 | 100.0 | 244 | 3 | US-09-140-804-3 | Sequence 3, Appi |
| 5 | 708 | 100.0 | 244 | 4 | US-09-336-536-20 | Sequence 20, Appi |
| 6 | 708 | 100.0 | 244 | 4 | US-09-530-423-1 | Sequence 1, Appi |
| 7 | 708 | 100.0 | 244 | 4 | US-09-886-838B-3 | Sequence 3, Appi |
| 8 | 708 | 100.0 | 244 | 4 | US-09-911-176B-4B | Sequence 4B, Appi |
| 9 | 708 | 100.0 | 244 | 4 | US-09-552-225A-3 | Sequence 3, Appi |
| 10 | 708 | 100.0 | 244 | 4 | US-09-619-140-51 | Sequence 51, Appi |
| 11 | 708 | 100.0 | 244 | 4 | US-09-776-976-6 | Sequence 6, Appi |
| 12 | 708 | 100.0 | 244 | 4 | US-09-909-547-6 | Sequence 6, Appi |
| 13 | 708 | 100.0 | 244 | 4 | US-09-569-852B-6 | Sequence 6, Appi |
| 14 | 708 | 100.0 | 244 | 4 | US-09-686-938B-8 | Sequence 3, Appi |
| 15 | 655 | 92.5 | 130 | 3 | US-09-485-316A-13 | Sequence 13, Appi |
| 16 | 655 | 92.5 | 247 | 2 | US-08-463-911-2 | Sequence 2, Appi |
| 17 | 655 | 92.5 | 247 | 3 | US-09-140-804-8 | Sequence 8, Appi |
| 18 | 655 | 92.5 | 247 | 3 | US-09-118-408-3 | Sequence 3, Appi |
| 19 | 655 | 92.5 | 247 | 4 | US-09-506-855-3 | Sequence 3, Appi |
| 20 | 655 | 92.5 | 247 | 4 | US-09-686-938B-8 | Sequence 8, Appi |
| 21 | 655 | 92.5 | 247 | 4 | US-09-911-176B-3 | Sequence 3, Appi |
| 22 | 655 | 92.5 | 247 | 4 | US-09-619-140-3 | Sequence 3, Appi |
| 23 | 655 | 92.5 | 247 | 4 | US-09-776-976-4 | Sequence 4, Appi |
| 24 | 655 | 92.5 | 247 | 4 | US-09-506-852-3 | Sequence 3, Appi |
| 25 | 655 | 92.5 | 247 | 4 | US-09-909-547-4 | Sequence 4, Appi |
| 26 | 655 | 92.5 | 247 | 4 | US-10-392-706-3 | Sequence 3, Appi |
| 27 | 645 | 91.1 | 130 | 3 | US-09-485-316A-12 | Sequence 12, Appi |

GENERAL INFORMATION:
 PATENT NO.: 6461821
 APPLICANT: Otsuka Pharmaceutical Co., Ltd.
 TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a kit
 TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
 TITLE OF INVENTION: therefore
 FILE REFERENCE: P98-51
 CURRENT APPLICATION NUMBER: US/09/530,423
 CURRENT FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: JP H9-297569
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 2
 LENGTH: 231
 TYPE: PRT
 ORGANISM: Abdominal fat tissue from myoma uteri
 S-09-530-423-2

RESULT 3
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 Best Local Similarity 100.0%; Pred. No. 1.8e-79; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sequence 7, Application US/08463911
 Patent No. 5869330

GENERAL INFORMATION:
 APPLICANT: Scherer, Philipp E.
 APPLICANT: Lodish, Harvey F.
 TITLE OF INVENTION: A NOVEL SERUM PROTEIN PRODUCED
 TITLE OF INVENTION: EXCLUSIVELY IN ADIPOCYTES
 NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
 STREET: Two Militia Drive
 CITY: Lexington
 STATE: Massachusetts
 COUNTRY: USA
 ZIP: 02173

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/463,911
 FILING DATE: 1997-08-26

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
 NAME: Granahan, Patricia
 REGISTRATION NUMBER: 32,227
 REFERENCE/DOCKET NUMBER: WHI95-05
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 861-6240
 TELEFAX: (617) 861-9540
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 244 amino acids

RESULT 4
 Query Match 100.0%; Score 708; DB 2; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.9e-79; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sequence 3, Application US/09140804
 Patent No. 6197930

GENERAL INFORMATION:
 APPLICANT: Sheppard, Paul O.
 APPLICANT: Humes, Jacqueline M.
 TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOGS
 FILE REFERENCE: 97-49
 CURRENT APPLICATION NUMBER: US/09/140,804
 CURRENT FILING DATE: 1998-08-26
 PRIOR APPLICATION NUMBER: 60/056,983
 EARLIER FILING DATE: 1997-08-26
 NUMBER OF SEQ ID NOS: 47
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 3
 LENGTH: 244
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-140-804-3

RESULT 5
 Query Match 100.0%; Score 708; DB 3; Length 244;
 Best Local Similarity 100.0%; Pred. No. 1.9e-79; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Sequence 20, Application US/09336536
 Patent No. 6406884

GENERAL INFORMATION:
 APPLICANT: Leiby, K.
 APPLICANT: McKay, C.
 APPLICANT: Bosone, S.

TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
 FILE REFERENCE: 7853-14
 CURRENT APPLICATION NUMBER: US/09/336,536
 CURRENT FILING DATE: 1999-06-18
 NUMBER OF SEQ ID NOS: 75
 SOFTWARE: PatentIn Ver. 2.0

MOLECULE TYPE: protein
 TOPOLOGY: linear
 US-08-463-911-7


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; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP3
; FILE REFERENCE: 99-09
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130,199
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO: 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-225A-3

Query Match 100.0%: Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 115 FSVGLETTYVTPNMPIRPKIFYNQNYHDGSTGKPHCNIPGLYFAVHTVMDKVVS 174
Qy 61 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 120
Db 175 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 234
Qy 121 TGFLLYHDTN 130
Db 235 TGFLLYHDTN 244

RESULT 10
US-09-619-740-51
Sequence 51, Application US/09619740
; Sequence 51, Application US/09619740
; Patent No. 65544946
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lasser, Gerald W.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: INHIBITORS FOR USE IN HEMOSTASIS AND IMMUNE FUNCTION
; CURRENT FILING DATE: 99-12-23
; FILE REFERENCE: 99-12-23
; CURRENT APPLICATION NUMBER: US/09/619,740
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/253,604
; PRIOR FILING DATE: 1999-02-19
; PRIOR APPLICATION NUMBER: 09/444,794
; PRIOR FILING DATE: 1999-11-22
; PRIOR APPLICATION NUMBER: 09/506,855
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 55
; SEQ ID NO: 51
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-619-740-51

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Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSVGLETTYVTPNMPIRPKIFYNQNYHDGSTGKPHCNIPGLYFAVHTVMDKVVS 60
Db 115 FSVGLETTYVTPNMPIRPKIFYNQNYHDGSTGKPHCNIPGLYFAVHTVMDKVVS 174
Qy 61 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 120
Db 175 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 234
Qy 121 TGFLLYHDTN 130
Db 235 TGFLLYHDTN 244

RESULT 11
US-09-776-976-6
Sequence 6, Application US/09776976
; Sequence 6, Application US/09776976
; Patent No. 6556332
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Binain, Bernard
; APPLICANT: Yen, Frances
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US/09/776,376
; CURRENT FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; CURRENT FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/176,228
; CURRENT FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 60/198,087
; CURRENT FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO: 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-776-976-6

Query Match 100.0%: Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1.9e-79; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 PSVGLETTYVTPNMPIRPKIFYNQNYHDGSTGKPHCNIPGLYFAVHTVMDKVVS 60
Db 115 FSVGLETTYVTPNMPIRPKIFYNQNYHDGSTGKPHCNIPGLYFAVHTVMDKVVS 174
Qy 61 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 120
Db 175 LFKKOKAMLFYDQYQENNDQASGSVLLHLEVGQWVQVYGEGERGLYADNDNSTF 234
Qy 121 TGFLLYHDTN 130
Db 235 TGFLLYHDTN 244

RESULT 12
US-09-909-547-6
Sequence 6, Application US/09909547
; Sequence 6, Application US/09909547
; Patent No. 6579832
; GENERAL INFORMATION:
; APPLICANT: Fruebis, Joachim
; APPLICANT: Erickson, Mary Ruth
; APPLICANT: Yen, Frances
; APPLICANT: Binain, Bernard
; TITLE OF INVENTION: OBG3 Globular Head and Uses Thereof for Decreasing Body Mass
; FILE REFERENCE: 76-US6.CIP
; CURRENT FILING DATE: 2001-07-19
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 09/776,976
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: US 09/758,055
; PRIOR FILING DATE: 2001-01-10
; PRIOR APPLICATION NUMBER: US 60/299,881
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: US 60/198,087
; PRIOR FILING DATE: 2000-04-13
; PRIOR APPLICATION NUMBER: US 60/176,228
; PRIOR FILING DATE: 2000-01-14

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; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent.pm
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-909-547-6

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Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 130
; Sequence 6, Application US/09569852B
; Patent No. 6592909
; GENERAL INFORMATION:
; APPLICANT: Bougueret, Lydie
; APPLICANT: Bihain, Bernard
; APPLICANT: Denon, Blake
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: APM1 Biallelic Markers and Uses Thereof
; FILE REFERENCE: GEN-T113XC2
; CURRENT APPLICATION NUMBER: US/09/569, 852B
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: PCT/IB99/0158
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 09/434, 848
; PRIOR FILING DATE: 1999-11-04
; PRIOR APPLICATION NUMBER: US 60/119, 593
; PRIOR FILING DATE: 1999-02-10
; PRIOR APPLICATION NUMBER: US 60/107, 113
; PRIOR FILING DATE: 1998-11-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: mbc feature
; LOCATION: (15)..(15) The 'Xaa' at location 15 stands for Gly.
; OTHER INFORMATION: NAME/KEY: mbc feature
; LOCATION: (1)..(367) OTHER INFORMATION: homology with 5' EST A254990 in private bank : GENSET
; NAME/KEY: mbc feature
; LOCATION: (91)..(93) OTHER INFORMATION: Amino acid at position 15 (Xaa) means Gly
; LOCATION: (15)..(15) OTHER INFORMATION: The 'Xaa' at location 15 stands for Gly.
; US-09-909-852B-6

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 130
; Sequence 13, Application US/09485316A
; Patent No. 634441
; GENERAL INFORMATION:
; APPLICANT: Bougueret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET-036AC
; CURRENT APPLICATION NUMBER: US/09/485, 316A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT 1198/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 130
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-485-316A-13

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 130
; Sequence 13, Application US/09485316A
; Patent No. 634441
; GENERAL INFORMATION:
; APPLICANT: Bougueret, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET-036AC
; CURRENT APPLICATION NUMBER: US/09/485, 316A
; CURRENT FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT 1198/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 130
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Mus musculus
; US-09-552-204A-3

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 130
; Sequence 3, Application US/09552204A
; Patent No. 6620909
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
; FILE REFERENCE: 93-08
; CURRENT APPLICATION NUMBER: US/09/552, 204A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130, 207
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-204A-3

Query Match 100.0%; Score 708; DB 4; Length 244;
Best Local Similarity 100.0%; Pred. No. 1. 9e-79;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; SEQ ID NO 130
; Sequence 3, Application US/09552204A
; Patent No. 6620909
; GENERAL INFORMATION:
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Bishop, Paul D.
; TITLE OF INVENTION: ADIPOCYTE-SPECIFIC PROTEIN HOMOLOG ZACRP2
; FILE REFERENCE: 93-08
; CURRENT APPLICATION NUMBER: US/09/552, 204A
; CURRENT FILING DATE: 2000-04-19
; PRIOR APPLICATION NUMBER: 60/130, 207
; PRIOR FILING DATE: 1999-04-20
; NUMBER OF SEQ ID NOS: 20
; SEQ ID NO 3
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-552-204A-3

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; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 118..267 of translation from ref genbank U37222
; US-09-485-316A-13

Query Match 92.5%; Score 655; DB 3; Length 130;
Best local Similarity 91.5%; Pred. No. 2.9e-73; Mismatches 4; Indels 0; Gaps 0;
Matches 119; Conservative 7; Mismatches 4; Indels 0; Gaps 0;

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Db 1 FSVGLEYTRVTPNVPIRFTKIFYNGDHYGSTGKFCNIEFLGLYFPSYHITVYMKDVKS 60
QY 61 LPKKOKAMFLTYDQENNTDQASSVLUHLEVGQWMLQVYGEGERGLYADNDSTP 120
Db 61 LPKKOKAVLFLTYDQEBKNTDQASGSVLUHLEVGQWMLQVYGDQGDHNGLYADNDSTP 120
QY 121 TGFLIXHDTN 130
Db 121 TGFLIXHDTN 130

Search completed: May 6, 2005, 17:33:03
Job time : 17.8027 secs

GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.

Copyright (c) 1993 - 2003 Compugen Ltd.

סמלים וסמלים (ג) 1993 - 2003

OM protein - protein search, using sw model

(without alignment) 652.420 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708

sequence: 1 FSVGLEYVITIPNMPRETK..... YABDNBDSTTGFLLYHBTN 130

According to the following table:
Biosensor 2
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

minimum DB seq length: 0
maximum DB seq length: 200000000

post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

database : A_Geneseq_16dec04:*

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2: geneseqP1998B:*
3: geneseqP2000B:*
4: geneseq2001B:*
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6: geneseqP2003as:*
7: geneseqP2003bs:*
8: geneseqD2004as:*
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Score. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

| No. | Score | Match | Length | DB | ID |
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|-----|-------|-------|--------|----|----|

1 708 100.0 130 2 AAY01485 Aay01485 Apml prc

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| | | | | | | |
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| 2 | 708 | 100.0 | 130 | 7 | ADE93609 | Ace93609 |
| 3 | 708 | 100.0 | 137 | 7 | ADE93608 | Ace93608 |
| 4 | 708 | 100.0 | 144 | 7 | ADE93607 | Ace93607 |
| 5 | 708 | 100.0 | 145 | 7 | ADE93613 | Ace93613 |
| 6 | 708 | 100.0 | 157 | 7 | ADE93610 | Ace93610 |
| 7 | 708 | 100.0 | 163 | 7 | ADE93612 | Ace93612 |
| 8 | 708 | 100.0 | 163 | 7 | ADE93655 | Ace93655 |
| 9 | 708 | 100.0 | 187 | 7 | ADE93615 | Ace93615 |
| 10 | 708 | 100.0 | 193 | 7 | ADE93614 | Ace93614 |
| 11 | 708 | 100.0 | 203 | 7 | ADE93605 | Ace93605 |
| 12 | 708 | 100.0 | 226 | 7 | ADE93604 | Ace93604 |
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| 15 | 708 | 100.0 | 233 | 7 | ADD93530 | Add93530_Novel_NG |
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| 18 | 708 | 100.0 | 244 | 3 | AYAY11035 | Acey11035_Human_Air |
| 19 | 708 | 100.0 | 244 | 3 | AAAB20233 | Abb30233_Human_adipose |
| 20 | 708 | 100.0 | 244 | 4 | AAAB65828 | Abb65828_Human_adipose |
| 21 | 708 | 100.0 | 244 | 4 | AAEB05529 | Aae05529_Human_adipose |
| 22 | 708 | 100.0 | 244 | 4 | AAAB49598 | Aceab49598_Human_AC |
| 23 | 708 | 100.0 | 244 | 4 | AAAB50373 | Aab50373_Human_acid |
| 24 | 708 | 100.0 | 244 | 4 | AAAB49592 | Aab49592_Human_AC |
| 25 | 708 | 100.0 | 244 | 5 | ABR08223 | Abbr08223_Human_AC |

CC having binding specificity for a gamma subunit of the lipolysis
 CC stimulated receptor (LSR) or a gC1q.R or gC1q.R homologue can be used for
 CC treatment of obesity, where the polypeptide is not a subunit of the LSR.
 CC The agents which increase partitioning of dietary lipids to the liver can
 CC be used for treating obesity-related hypertension, microangiopathic lesions
 CC insulin resistance, obesity-related hypertriglyceridemia, obesity-related
 CC resulting from obesity-related Type II diabetes, ocular lesions caused by
 CC microangiopathy in obese individuals with Type II diabetes, and renal
 CC lesions caused by microangiopathy in obese individuals with Type II
 CC diabetes. Agents which decrease the partitioning of dietary lipids to the
 CC liver can be used for treating cachexia in subjects with neoplastic or
 CC para-neoplastic syndrome or eating disorders. The present sequence
 CC represents a claimed peptide fragment of apm1.

SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 2; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60
 DB 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60

QY 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120
 DB 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120

QY 121 TGFLLYHDTN 130
 DB 121 TGFLLYHDTN 130

SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 7; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60
 DB 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60

QY 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120
 DB 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120

DE Human adiponectin apm1(115-244) protein.
 XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antiheumatic; antibacterial; antiipaemic; dermatological; anorectic;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis; myocardial
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

PN WO2003055916-A2.

XX 10-JUL-2003.

PD 20-DEC-2002; 2002WO-DK000897.

XX 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00006227.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-0001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI PI Bognsæs A;

XX WPI; 2003-598262/56.

PR New conjugate comprising an adiponectin polypeptide and a first non-
 PR polypeptide moiety, useful for preparing a composition for treating a
 PR mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

XX Claim 14; SEQ ID NO 7; 184pp; English.

PS The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 CC acid residue having an attachment group for the first non-polypeptide
 moiety which has been introduced in a position where the parent
 CC conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apm1 protein of the
 CC invention.

SQ Sequence 130 AA;

Query Match 100.0%; Score 708; DB 7; Length 130;
 Best Local Similarity 100.0%; Pred. No. 3.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60
 DB 1 PSVGLENYVTIPNMPIRFTKIFYNQONHYDSTGKFCNIPGLYFAVHITVYMKDVKS 60

QY 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120
 DB 61 LFKKOKAMLFYDQYQENNVDQASGSVLLHLEVGQWMLQVYGERGLYADNDNSTP 120

QY 121 TGFLLYHDTN 130
 DB 121 TGFLLYHDTN 130

DE Human adiponectin apm1(108-244) protein.
 XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antiheumatic; antibacterial; antiipaemic; dermatological; anorectic;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.

XX Homo sapiens.

OS WO2003055916-A2.

XX 10-JUL-2003.

PD 20-DEC-2002; 2002WO-DK000897.

XX 21-DEC-2001; 2001US-0343482P.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00006227.

PR 25-APR-2002; 2002US-0375492P.

PR 03-JUL-2002; 2002DK-0001036.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;

PI PI Bognsæs A;

XX WO2003055916-A2.

XX 10-JUL-2003.

PD 20-DEC-2002; 2002WO-DK000897.

XX 21-DEC-2001; 2001DK-00001952.
 PR KW
 PR 21-DEC-2001; 2001US-0343482P.
 PR KW
 PR 25-APR-2002; 2002DK-00000627.
 PR KW
 PR 25-APR-2002; 2002US-0375492P.
 PR KW
 PR 03-JUL-2002; 2002DK-00001036.
 PR KW
 PR 03-JUL-2002; 2002US-0394117P.
 PR KW
 PR 20-SEP-2002; 2002DK-00001385.
 PR KW
 PR 20-SEP-2002; 2002US-0412169P.
 PA KW
 PA (MAXY-) MAXYGEN APS.
 PA KW
 XX Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PT Bognes A;
 XX DR WPI; 2003-598262/56:
 PT New conjugate comprising an adiponectin polypeptide and a first non-
 PT polypeptide moiety, useful for preparing a composition for treating a
 PT mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.
 XX PS Claim 14; SEQ ID NO 6; 184pp; English.
 XX CC
 CC The invention relates to a novel conjugate comprising an adiponectin
 CC polypeptide and a first non-polypeptide moiety covalently attached to the
 CC adiponectin polypeptide. The adiponectin polypeptide comprises an amino
 acid residue having an attachment group for the first non-polypeptide
 CC moiety which has been introduced in a position where the parent
 CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiatherosclerotic, anti-diabetic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity, atherosclerosis,
 CC cardiovascular diseases, dyslipidemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC current sequence is that of the human adiponectin apm1 protein of the
 CC invention.
 XX SQ Sequence 137 AA:
 Query Match 100.0%; Score 708; DB 7; Length 137;
 Best Local Similarity 100.0%; Pred. No. 3.8e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 60
 Db 8 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 67
 Qy 61 LFKKDKKAMLFYDQYQENNDQASGSVVLHLEVGDQWLVQVYGEGERGLYADNDNSTF 120
 Db 68 LFKKDKKAMLFYDQYQENNDQASGSVVLHLEVGDQWLVQVYGEGERGLYADNDNSTF 127
 Qy 121 TGFLLYHDTN 130
 Db 128 TGFLLYHDTN 137
 RESULT 4
 ADE9307 Best Local Similarity 100.0%; Score 708; DB 7; Length 144;
 ID ADE93607 Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX SQ Sequence 144 AA:
 Query Match 100.0%; Score 708; DB 7; Length 144;
 Best Local Similarity 100.0%; Pred. No. 4.1e-78;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 60
 Db 15 FSVGLEYTVTIPNMPIRTKIFYNQHNYDGSTGKFCNPIGLYFAHYITVYMKDVKVS 74
 Qy 61 LFKKDKKAMLFYDQYQENNDQASGSVVLHLEVGDQWLVQVYGEGERGLYADNDNSTF 120
 Db 75 LFKKDKKAMLFYDQYQENNDQASGSVVLHLEVGDQWLVQVYGEGERGLYADNDNSTF 134
 Qy 121 TGFLLYHDTN 130
 Db 135 TGFLLYHDTN 144
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.
 XX OS Homo sapiens.
 XX PN WO2003055916-A2.
 XX PD 10-JUL-2003.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
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 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
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 XX PA (MAXY-) MAXYGEN APS.
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 XX PA (MAXY-) MAXYGEN APS.
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 XX PA (MAXY-) MAXYGEN APS.
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 PR 25-APR-2002; 2002US-0375492P.
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 PR 03-JUL-2002; 2002US-0394117P.
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 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
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 PR 20-SEP-2002; 2002US-0412169P.
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 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
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 PR 03-JUL-2002; 2002US-0394117P.
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 PR 20-SEP-2002; 2002US-0412169P.
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 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
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 PR 03-JUL-2002; 2002US-0394117P.
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 PR 20-SEP-2002; 2002US-0412169P.
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 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
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 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
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 PR 21-DEC-2001; 2001US-0343482P.
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 PR 03-JUL-2002; 2002US-0394117P.
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 PR 21-DEC-2001; 2001US-0343482P.
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 PR 25-APR-2002; 2002US-0375492P.
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 PR 03-JUL-2002; 2002US-0394117P.
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 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
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 XX PR 21-DEC-2001; 2001DK-00001952.
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 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
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 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
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 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
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 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
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 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
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 XX PA (MAXY-) MAXYGEN APS.
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 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK-00001316.
 PR 03-JUL-2002; 2002US-0394117P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX PA (MAXY-) MAXYGEN APS.
 XX PR 20-DEC-2002; 2002WO-DK000897.
 XX PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 25-APR-2002; 2002US-0375492P.
 PR 03-JUL-2002; 2002DK

RESULT 5
 ADE93613
 ID ADE93613 standard; protein; 145 AA.
 XX
 AC ADE93613;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human adiponectin apm1(100-244) protein.
 KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW anti-rheumatic; antibacterial; antiipaemic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.
 OS Homo sapiens.
 XX
 PN WO2003055916-A2.
 XX
 PD 10-JUL-2003.
 XX
 PP 20-DEC-2002; 2002WO-DK000897.
 XX
 PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0374492P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bognes A;
 XX
 DR WPI; 2003-598262/56.

New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

Claim 44; SEQ ID NO 11; 184pp; English.

The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic, cardiant, antineumatic, antibacterial, antiipaemic, dermatological, immunosuppressive, immunomodulator and anorectic activities and may be useful for treating diabetes, obesity, atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid arthritis, Crohn's disease, systemic lupus erythematosus, sjogren syndrome, cachexia, septic shock, myasthenia gravis, myocardial infarction and destructive processes related to activation of the inflammatory system, as well as during gene therapy procedures. The current sequence is that of the human adiponectin apm1 protein of the invention.

Sequence 145 AA:

100.0%; Score 708; DB 7; Length 145;

Query 1 PSVGLETTYWIPNPPIRFTKIFQYQNTGDSKFKHNPGLYFYAHITVWMDKVS 60
 Database 16 PSVGLETTYWIPNPPIRFTKIFQYQNTGDSKFKHNPGLYFYAHITVWMDKVS 75
 Query 61 LFKKDKAMLYTYDQYQENNDQASGSVLLHLEVGDQVWQVYGERNGIYADNDNSTR 120
 Database 76 LFKKDKAMLYTYDQYQENNDQASGSVLLHLEVGDQVWQVYGERNGIYADNDNSTR 135
 Query 121 TGFLLYHDTN 130
 Database 136 TGFLLYHDTN 145

RESULT 6
 ADE93606 standard; protein; 157 AA.
 XX
 AC ADE93606;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Human adiponectin apm1(88-244) protein.
 KW adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW anti-rheumatic; antibacterial; antilipaemic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type.
 OS Homo sapiens.
 XX
 PN WO2003055916-A2.
 XX
 PD 10-JUL-2003.
 XX
 PR 20-DEC-2002; 2002WO-DK000897.
 XX
 PR 21-DEC-2001; 2001DK-00001952.
 PR 21-DEC-2001; 2001US-0343482P.
 PR 25-APR-2002; 2002DK-00000627.
 PR 03-JUL-2002; 2002US-0374492P.
 PR 03-JUL-2002; 2002DK-00001036.
 PR 03-JUL-2002; 2002US-0374492P.
 PR 20-SEP-2002; 2002DK-00001385.
 PR 20-SEP-2002; 2002US-0412169P.
 XX
 PA (MAXY-) MAXYGEN APS.
 PA (MAXY-) MAXYGEN HOLDINGS LTD.
 XX
 PI Rasmussen PB, Andersen KV, Pedersen AH, Schambye HT, Halkier T;
 PI Bognes A;
 XX
 DR WPI; 2003-598262/56.

New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

Claim 44; SEQ ID NO 4; 184pp; English.

The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic,

CC adiponectin is occupied by a surface exposed amino acid residue. The
 CC conjugate of the invention demonstrates antiarteriosclerotic,
 CC anti-diabetic, cardiant, anti-rheumatic, anti-bacterial, anti-lipaemic,
 CC dermatological, immunosuppressive, immunomodulator and anorectic
 CC activities and may be useful for treating diabetes, obesity,
 CC arteriosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid
 CC arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren
 CC syndrome, cachexia, septic shock, myasthenia gravis, myocardial
 CC infarction and destructive processes related to activation of the
 CC inflammatory system, as well as during gene therapy procedures. The
 CC current sequence is that of the human adiponectin apm1 protein of the
 CC invention.
 XX

SQ Sequence 203 AA;

Query Match 100.0%; Score 708; DB 7; Length 203;
 Best Local Similarity 100.0%; Pred. No. 6.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; NtMatches 0; Pairs 0;

QY 1 PSVGLETYVTIPNMPIRFTKLYFQYQHNTVYMDKVVS 60
 DB 74 PSVGLETYVTIPNMPIRFTKLYFQYQHNTVYMDKVVS 133

QY 61 LFKKDKAMLFYTDQYQENNNQDASGVVLIHEVGQWMLQVYGERNRGLYADNDNST 120
 DB 134 LFKKDKAMLFYTDQYQENNNQDASGVVLIHEVGQWMLQVYGERNRGLYADNDNST 193

QY 121 TGFLIYHDTN 130
 DB 194 TGFLIYHDTN 203

RESULT 12

ID ADE93604

ID ADE93604 standard; protein; 226 AA.

AC ADE93604;

DT 12-FEB-2004 (first entry)

XX Human adiponectin apm1 (19-244) protein.

XX adiponectin conjugate; antiarteriosclerotic; antidiabetic; cardiant;
 KW antiheumatic; antimicrobial; antilipaemic; dermatological;
 KW immunosuppressive; immunomodulator; anorectic; diabetes; obesity;
 KW atherosclerosis; cardiovascular disease; dyslipidaemia;
 KW rheumatoid arthritis; Crohn's; systemic lupus erythematosus;
 KW Sjogren syndrome; cachexia; septic shock; myasthenia gravis;
 KW myocardial infarction; inflammation; gene therapy; human; apm1;
 KW wild-type; wild-type.

OS Homo sapiens.

PN WO2003055916-A2.

XX 10-JUL-2003.

PD 20-DEC-2002; 2002WO-DK000897.

XX PR 21-DEC-2001; 2001DK-00001952.

PR 21-DEC-2001; 2001US-0343482P.

PR 25-APR-2002; 2002DK-00000627.

PR 03-JUL-2002; 2002DK-000103.

PR 03-JUL-2002; 2002US-0394117P.

PR 20-SEP-2002; 2002DK-00001385.

PR 20-SEP-2002; 2002US-0412169P.

XX PA (MAXY-) MAXYGEN APS.

PA (MAXY-) MAXYGEN HOLDINGS LTD.

PI Rasmussen PB, Andersen KV, Pedersen AH, Schambrey HT, Halkier T;

XX Matsuzawa Y, Ohmoto Y;

WPI; 2003-598262/56.

DR

XX New conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety, useful for preparing a composition for treating a mammal having e.g., diabetes, atherosclerosis or cardiovascular disease.

PT

XX Pairs

XX Claim 14; SEQ ID NO 2; 184pp; English.

XX

CC The invention relates to a novel conjugate comprising an adiponectin polypeptide and a first non-polypeptide moiety covalently attached to the adiponectin polypeptide. The adiponectin polypeptide comprises an amino acid residue having an attachment group for the first non-polypeptide moiety which has been introduced in a position where the parent adiponectin is occupied by a surface exposed amino acid residue. The conjugate of the invention demonstrates antiarteriosclerotic, antidiabetic, cardiant, anti-rheumatic, anti-bacterial, anti-lipaemic, dermatological, immunosuppressive, immunomodulator and anorectic activities and may be useful for treating diabetes, obesity, atherosclerosis, cardiovascular diseases, dyslipidaemia, rheumatoid arthritis, Crohn's disease, systemic lupus erythematosus, Sjogren syndrome, cachexia, septic shock, myasthenia gravis, myocardial infarction and destructive processes related to activation of the inflammatory system, as well as during gene therapy procedures. The current sequence is that of the human adiponectin apm1 protein of the invention.

XX

SQ Sequence 226 AA;

Query Match 100.0%; Score 708; DB 7; Length 226;
 Best Local Similarity 100.0%; Pred. No. 7.5e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; NtMatches 0; Pairs 0;

QY 1 PSVGLETYVTIPNMPIRFTKLYFQYQHNTVYMDKVVS 60
 DB 97 PSVGLETYVTIPNMPIRFTKLYFQYQHNTVYMDKVVS 156

QY 61 LFKKDKAMLFYTDQYQENNNQDASGVVLIHEVGQWMLQVYGERNRGLYADNDNST 120
 DB 157 LFKKDKAMLFYTDQYQENNNQDASGVVLIHEVGQWMLQVYGERNRGLYADNDNST 216

QY 121 TGFLIYHDTN 130
 DB 217 TGFLIYHDTN 226

RESULT 13

AY21808

ID AAY21808 standard; protein; 231 AA.

XX

AC AAY21808;

XX

DT 10-SEP-1999 (first entry)

XX

DE Adipose most abundant gene transcription product 1 (apm1) fragment.

XX Smooth muscle proliferation; secretion factor; apm1; adipose; adipose most abundant gene transcription product 1; obesity; arteriosclerosis; restenosis; angina pectoris; myocardial infarction.

XX Unidentified.

XX WO921577-A1.

XX

PD 06-MAY-1999.

XX

PP 27-OCT-1998; 98W0-JP004862.

XX

BR 29-OCT-1997; 97JP-00297569.

XX

PA (SAKA) OTSUKA PHARM CO LTD.

XX

PI Matsuzawa Y, Ohmoto Y;

XX
DR WPI; 1999-418412/35.

XX
PT Inhibition of smooth muscle proliferation using secretion factor apm1.

XX
PS Example; Page 59-60; 65pp; Japanese.

Then invention relates to the inhibition of smooth muscle proliferation using a composition containing secretion factor apm1 (adipose most abundant gene transcript product 1), together with a suitable carrier. apm1 is expressed specifically in adipose tissue and the composition is used for the prevention and treatment of arteriosclerosis; restenosis following vascular reconstruction; and treatment and diagnosis of diseases related to obesity, and disorders associated with it such as angina pectoris and myocardial infarction. The present sequence represents a fragment of apm1 isolated from abdominal fat tissue of myoma uteri.

XX
SQ Sequence 231 AA;

Query Match 100.0%; Score 708; DB 2; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.8e-78; Mismatches 0; Indels 0; Gaps 0;

Matches 130; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

method comprises boiling the sample containing the antigenic protein in the presence of Sodium sulphate, diluting it in buffer, and detecting the enzyme by enzyme-linked immunosorbent assay (ELISA). In an exemplification of the invention, residues 15-244 (plus an initial Met residue) of human apm1 (adipose most abundant gene transcript 1; AAB60347), an adipose-specific collagen-like factor, was recombinantly expressed in *Escherichia coli*. Using the method of the invention, it was found that apm1 was expressed mainly in the inclusion body fragment as an approximately 30 kd protein. The present sequence represents the recombinantly expressed human apm1.

Sequence 231 AA;

Query Match 100.0%; Score 708; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 7.8e-78; Mismatches 0; Indels 0; Gaps 0;
Matches 130; Conservative 0; MisMatches 0; Indels 0; Gaps 0;

QY 1 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60
Db 102 FSVGLETIVTIPNMPIRFKIFPQNQHGSTOKPHCNIPGLYFAHITVVKDKVKS 60

QY 61 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120
Db 162 LFKKDKAMLFITYDQYQENNDQASGSVILHLEVGDQWNLQVYGERGNGLYAENDNSTF 120

QY 121 TGFLILYHDIN 130
Db 222 TGFLILYHDIN 231

RESULT 15
ID ADD93530
ID ADD93530 standard; protein; 233 AA.
AC ADD93530;
AC ADD93530;
DT 28-JAN-2004 (first entry)
XX
DE Novel NOV2e, homologous to human adiponectin.
XX
KW NOV2e; human; adiponectin; gene therapy.
XX
OS Homo sapiens.
XX
PN W02003078572-A2.
XX
PD 25-SEP-2003.
XX
PF 06-MAR-2003; 2003WO-US006659.
XX
PR 15-MAR-2002; 2002US-0365034P.
PR 19-MAR-2002; 2002US-0365477P.
PR 21-MAR-2002; 2002US-0366420P.
PR 05-MAR-2003; 2003US-00379747.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Burgess CE, Chant JS, Chaudhuri A, Edinger SR, Gangolli EA;
PI Malyankar UM, Miller CE, Ooi CE, Ort T, Paturrajan M, Rastelli L;
PI Rieger DK, Shinkets RA, Zerhusen BD;
XX
DR WPI; 2003-779122/73.
XX
DR N-PSDB; ADD93529.

New isolated NOV2 polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOV2-associated disorderB, e.g., osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.

Claim 1; Page 108; 205pp; English.

The present sequence is the protein sequence of a novel polypeptide, designated NOV2, that shows amino acid sequence homology to the human

CC adiponectin (adipose most abundant gene transcript 1, APM1). The
 CC adiponectin gene is the most abundant gene transcript in adipose cells
 CC that regulates lipid metabolism. An interaction between adiponectin and
 CC calcium modulating ligand was identified, indicating a novel pathway by
 CC which adiponectin may induce lipid breakdown in muscle cells and
 CC adipocytes. The invention is based on the identification of proteins and
 CC polypeptides, and the nucleic acids encoding them, that are
 CC differentially modulated in a pathological state, disease or an abnormal
 CC condition or state. These are targets for therapeutic agents and can be
 CC used in screening methodologies to identify candidate therapeutic agents
 CC which interact with the target and thereby exert a desired or favourable
 CC effect, e.g. in neurogenesis, cell differentiation, cell proliferation,
 CC haemopoiesis, wound healing and angiogenesis. Methods for diagnosis,
 CC treatment and prevention of disorders involving the novel human nucleic
 CC acids and proteins are provided. The polypeptides are also used to raise
 CC antibodies, useful in therapy and diagnosis.
 XX

SQ Sequence 233 AA:

Query Match 100 %; Score 708; DB 7; Length 233;
 Best Local Similarity 100 %; Pred. No. 7. 9e-78; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
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| QY | 1 | PSVGLIETYVTPNMPIRFTKIFYNQDNHYDSTGKHCNTPGLYTFAYHITVYMKDVKS | 60 |
| Db | 104 | PSVGLIETYVTPNMPIRFTKIFYNQDNHYDSTGKHCNTPGLYTFAYHITVYMKDVKS | 163 |
| QY | 61 | LFKKDQAMLFYDQOENNVQASGVLLHEVGDQWLQTYGEGERGLYIADNDNSTF | 120 |
| Db | 164 | LFKKDQAMLFYDQOENNVQASGVLLHEVGDQWLQTYGEGERGLYIADNDNSTF | 223 |
| QY | 121 | TGFLLYHDTN | 130 |
| Db | 224 | TGFLLYHDTN | 233 |

Search completed: May 6, 2005, 17:22:12
 Job time : 79.0651 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: May 8, 2005, 13:27:58 ; Search time 55.967 Seconds
(without alignment)
774.883 Million cell updates/sec

Title: US-10-072-159-11

Perfect score: 708

Sequence: 1 FSVGLETVTIPNMPIRFTK..... YADNDNDSTPTGFLLYHDTN 130

Scoring table: BL05H62

Gapext 10.0 , Gapext 0.5

Searched: 1428581 seqs, 33359853 residues

Total number of hits satisfying chosen parameters: 1428581

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|-------|----------------------|
| 1 | 708 | 100.0 | 130 | 13 US-10-072-159-11 |
| 2 | 708 | 100.0 | 130 | 13 US-10-060-845-11 |
| 3 | 708 | 100.0 | 130 | 14 US-10-325-717-7 |
| 4 | 708 | 100.0 | 137 | 14 US-10-325-717-6 |
| 5 | 708 | 100.0 | 144 | 14 US-10-325-717-5 |
| 6 | 708 | 100.0 | 145 | 14 US-10-325-717-11 |
| 7 | 708 | 100.0 | 157 | 14 US-10-325-717-4 |
| 8 | 708 | 100.0 | 160 | 17 US-10-559-782A-23 |
| 9 | 708 | 100.0 | 163 | 14 US-10-325-717-10 |
| 10 | 708 | 100.0 | 163 | 14 US-10-325-717-53 |
| 11 | 708 | 100.0 | 187 | 14 US-10-325-717-13 |
| 12 | 708 | 100.0 | 193 | 14 US-10-325-717-12 |
| 13 | 708 | 100.0 | 203 | 14 US-10-325-717-3 |

QV

QV

RESULT 1
US-10-072-159-11
; Sequence 11, Application US/10072159
; Publication No. US20020151498A1
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougueret, Lydie
; APPLICANT: Yen-Potin, Fran^cois
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; FILE REFERENCE: GENSET 036AC
; CURRENT APPLICATION NUMBER: US/10/072-159
; CURRENT FILING DATE: 2002-02-05
; PRIORITY APPLICATION NUMBER: 02/485,316
; PRIORITY FILING DATE: 2000-02-04
; PRIORITY APPLICATION NUMBER: FR 98/05032
; PRIORITY FILING DATE: 1998-04-22
; PRIORITY APPLICATION NUMBER: PCT 1998/01256
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent-pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371
US-10-072-159-11
Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 4.4e-70;
Matches 130; Conservative 0; Mismatches 0; Index 0; Gaps 0;
Sequence 1, Appli
Sequence 2, Appli
Sequence 3, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 11, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 14, Appli
Sequence 15, Appli
Sequence 16, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 20, Appli
Sequence 21, Appli
Sequence 22, Appli
Sequence 23, Appli
Sequence 24, Appli
Sequence 25, Appli
Sequence 26, Appli
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Sequence 92, Appli
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Sequence 94, Appli
Sequence 95, Appli
Sequence 96, Appli
Sequence 97, Appli
Sequence 98, Appli
Sequence 99, Appli
Sequence 100, Appli
Sequence 101, Appli
Sequence 102, Appli
Sequence 103, Appli
Sequence 104, Appli
Sequence 105, Appli
Sequence 106, Appli
Sequence 107, Appli
Sequence 108, Appli
Sequence 109, Appli
Sequence 110, Appli
Sequence 111, Appli
Sequence 112, Appli

RESULT 2
US-10-060-845-11
; Sequence 11, Application US/10060845
; Publication No. US20020165154A1
; GENERAL INFORMATION:
; APPLICANT: Bihain, Bernard
; APPLICANT: Bougnelert, Lydie
; APPLICANT: Yen-Potin, Frances
; TITLE OF INVENTION: Lipoprotein-regulating medicaments
; CURRENT APPLICATION NUMBER: US/10/060,845
; CURRENT FILING DATE: 2002-01-29
; CURRENT APPLICATION NUMBER: U.S. 09/485,316
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: PCT IB98/01256
; PRIOR FILING DATE: 1998-08-06
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent.pm
; SEQ ID NO 11
; LENGTH: 130
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: 1..130
; OTHER INFORMATION: fragment 115..244 of translation from ref Genbank D45371

Query Match 100.0%; Score 708; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 4..4e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FSVGLLETYVTPNMPIRFTKIFYNQONHYDOSTGKPHCNIPGLYFAVHITVYMKDVKS 60
1 FSVGLLETYVTPNMPIRFTKIFYNQONHYDOSTGKPHCNIPGLYFAVHITVYMKDVKS 60
Db 61 LFKKOKAMLFYDQVQENNVDQASGSVVLHLEVGQDQVNQVYGERGLYIADNDNSTR 120
QY 61 LFKKOKAMLFYDQVQENNVDQASGSVVLHLEVGQDQVNQVYGERGLYIADNDNSTR 120
Db 61 LFKKOKAMLFYDQVQENNVDQASGSVVLHLEVGQDQVNQVYGERGLYIADNDNSTR 120
QY 121 TGFLLYHDTN 130
Db 121 TGFLLYHDTN 130

RESULT 3
US-10-325-717-7
; Sequence 7, Application US/10325717
; Publication No. US20030176328A1
; GENERAL INFORMATION:
; APPLICANT: Rasmussen, Poul Baad
; APPLICANT: Andersen, Kim Vilbø
; APPLICANT: Andersen, Anders Hjelholt
; APPLICANT: Schambye, Hans Thalsgaard
; APPLICANT: Halkier, Torben
; APPLICANT: Bøgesøe, Are
; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
; FILE REFERENCE: 021518610
; CURRENT APPLICATION NUMBER: US/10/325,717
; CURRENT FILING DATE: 2002-12-20
; CURRENT APPLICATION NUMBER: US 60/412,169
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: US 60/394,117
; PRIOR FILING DATE: 2002-07-3
; PRIOR APPLICATION NUMBER: US 60/375,492
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: US 60/343,482
; PRIOR FILING DATE: 2001-12-21
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: OTHER INFORMATION: apm1(108-244)
; LOCATION: 1..137
; OTHER INFORMATION: apm1(108-244)

Query Match 100.0%; Score 708; DB 14; Length 137;
Best Local Similarity 100.0%; Pred. No. 4..7e-70;
Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: 0251ue610

QY 1 FSVGLETVVTIPNMPIRFTKIFQNQHNDGSTGKFFCNIPGLYFAVHITVNMKDVKVS 60
 ; APPLICANT: Bøgesøe, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0211us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 11
 ; LENGTH: 145
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: apM1(100-244)

RESULT 5
 US-10-325-717-5
 ; Sequence 5, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbør
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bøgesøe, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0211us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 5
 ; LENGTH: 144
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: apM1(101-244)

US-10-325-717-5
 Query Match Best Local Similarity 100.0%; Score 708; DB 14; length 144;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 FSVGLETVVTIPNMPIRFTKIFQNQHNDGSTGKFFCNIPGLYFAVHITVNMKDVKVS 60
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbør
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Bøgesøe, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0211us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FASTSEQ for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 157
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: apM1(88-244)

RESULT 6
 US-10-325-717-11
 ; Sequence 11, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbør
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard

Query Match 100.0%; Score 708; DB 14; Length 157;
 Best Local Similarity 100.0%; Pred. No. 5.5e-70;
 Matches 130; Conservative 0; Mismatches 0;
 Indels 0; Gaps 0;

1 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 60
 28 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 87

61 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 120
 88 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 147

121 TGFLIYHDTN 130
 148 TGFLIYHDTN 157

RESULT 8
 SEQ ID NO 23
 LENGTH: 160
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 SEQ ID NO 23
 LENGTH: 160
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 IS-10-659-782A-23

Query Match 100.0%; Score 708; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5.8e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 60
 34 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 93

61 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 120
 94 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 153

121 TGFLIYHDTN 130
 154 TGFLIYHDTN 163

RESULT 9
 SEQ ID NO 23
 LENGTH: 160
 TYPE: PRT
 ORGANISM: *Homo sapiens*
 IS-10-659-782A-23

Query Match 100.0%; Score 708; DB 17; Length 160;
 Best Local Similarity 100.0%; Pred. No. 5.7e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 60
 31 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 90

61 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 120
 91 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 150

121 TGFLIYHDTN 130
 151 TGFLIYHDTN 160

RESULT 10
 SEQ ID NO 53
 LENGTH: 163
 TYPE: PRT
 ORGANISM: *Artificial Sequence*
 IS-10-325-717-10

Query Match 100.0%; Score 708; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5.8e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 60
 34 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 93

61 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 120

121 TGFLIYHDTN 130
 154 TGFLIYHDTN 163

RESULT 11
 SEQ ID NO 53
 LENGTH: 163
 TYPE: PRT
 ORGANISM: *Artificial Sequence*
 IS-10-325-717-10

Query Match 100.0%; Score 708; DB 14; Length 163;
 Best Local Similarity 100.0%; Pred. No. 5.8e-70;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 60
 34 FSVGLETYVTIPNMPIRFTKIFYNQONHYDGSTGKFCNIPGLYFAVHITVMDKVKS 93

61 LFKKDKAMLFYDQOENNVDQASGSVLUHLLEVQDWLQVYGEGERNGLYADNDNDSTP 120

RESULT 11
 US-10-325-717-13
 ; Sequence 13, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbø
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bogense, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343,482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 12
 ; LENGTH: 193
 ; FEATURE:
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: apM1(52-244)
 ; US-10-325-717-13

Query Match 100.0%; Score 708; DB 14; Length 193;
 Best Local Similarity 100.0%; Pred. No. 7.2e-70; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGGLETVTIPNMPIRFTKIFNQNQHNDGSTGKHCNIPOLYLYFAHITYVMKVKS 60
 Db 64 FSVGGLETVTIPNMPIRFTKIFNQNQHNDGSTGKHCNIPOLYLYFAHITYVMKVKS 123
 Qy 61 LFKKDKKAMLFPTDQYQENNVDQASGVVLUHLLEVGDQWLNQVYGEGERGLYADNDNSTF 120
 Db 124 LFKKDKKAMLFPTDQYQENNVDQASGVVLUHLLEVGDQWLNQVYGEGERGLYADNDNSTF 183
 Qy 121 TGFLYHDTN 130
 Db 184 TGFLYHDTN 193

RESULT 12
 US-10-325-717-12
 ; Sequence 12, Application US/10325717
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rasmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilbø
 ; APPLICANT: Pedersen, Anders Hjelholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bogense, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325,717
 ; PRIOR FILING DATE: 2002-12-20
 ; PRIOR APPLICATION NUMBER: US 60/412,169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394,117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375,492
 ; PRIOR FILING DATE: 2002-04-25
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 203
 ; FEATURE:
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: apM1(42-244)
 ; US-10-325-717-3

Query Match 100.0%; Score 708; DB 14; Length 203;
 Best Local Similarity 100.0%; Pred. No. 7.6e-70; Mismatches 0; Indels 0; Gaps 0;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FSVGGLETVTIPNMPIRFTKIFNQNQHNDGSTGKHCNIPOLYLYFAHITYVMKVKS 60

RESULT 14
 US-10-325-717-2
 ; Sequence 2, Application US/10325/17
 ; Publication No. US20030176328A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Basmussen, Poul Baad
 ; APPLICANT: Andersen, Kim Vilborg
 ; APPLICANT: Pedersen, Anders Højholt
 ; APPLICANT: Schambye, Hans Thalsgaard
 ; APPLICANT: Halkier, Torben
 ; APPLICANT: Bøgesnes, Are
 ; TITLE OF INVENTION: Adiponectin Fragments and Conjugates
 ; FILE REFERENCE: 0251us610
 ; CURRENT APPLICATION NUMBER: US/10/325, 717
 ; CURRENT FILING DATE: 2002-12-20
 ; PRIORITY APPLICATION NUMBER: US 60/412, 169
 ; PRIOR FILING DATE: 2002-09-20
 ; PRIOR APPLICATION NUMBER: US 60/394, 117
 ; PRIOR FILING DATE: 2002-07-03
 ; PRIOR APPLICATION NUMBER: US 60/375, 492
 ; PRIOR FILING DATE: 2002-04-25
 ; PRIOR APPLICATION NUMBER: US 60/343, 482
 ; PRIOR FILING DATE: 2001-12-21
 ; NUMBER OF SEQ ID NOS: 115
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 2
 ; LENGTH: 226
 ; TYPE: PRT
 ; FEATURE:
 ; ORGANISM: Homo sapiens
 ; OTHER INFORMATION: apm1(19-244)
 ; US-10-325-717-2

Query Match 100.0%; Score 708; DB 14; Length 231;
 Beat Local Similarity 100.0%; Pred. No. 9e-70; DB Matches 0; MiBmatches 0; Indels 0; Gaps 0;

QY 1 PSVGLETYVTPNMPIRFTKIPYQHNGSTGKPHCNIPGLYVFAVHITVYMKDVKS 60
 Db 102 PSVGLETYVTPNMPIRFTKIPYQHNGSTGKPHCNIPGLYVFAVHITVYMKDVKS 161
 QY 61 LFKKOKAMLFYDQOENNVDQASGSVLLHLEVGDOVWLOQYGEGERNGLYADNDNSTF 120
 Db 162 LFKKOKAMLFYDQOENNVDQASGSVLLHLEVGDOVWLOQYGEGERNGLYADNDNSTF 221
 QY 121 TGFLIYHDTN 130
 Db 222 TGFLIYHDTN 231

Search completed: May 8, 2005, 15:47:33
 Job time : 56.967 secs

RESULT 15
 US-10-189-493-2
 ; Sequence 2, Application US/10189/93
 ; Publication No. US2003016651A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Otsuka Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: Smooth muscle growth inhibitory composition, a
 ; TITLE OF INVENTION: diagnostic method for arteriosclerosis and a kit
 ; TITLE OF INVENTION: therefore
 ; FILE REFERENCE: P98-51
 ; CURRENT APPLICATION NUMBER: US/10/189, 493

S23297
 collagen alpha 1(X) chain precursor - chicken
 N;Alternate names: type X collagen
 C;Species: Gallus gallus (chicken)
 C;Date: 07-Oct-1994 #sequence revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S23297; A31896; S55594; S77711; I50218
 R;Ninomiya, Y.; Castagnola, P.; Gercke, D.; Gordon, M.K.; Jacenko, O.; LuWalle, P.; MCC
 maguchi, N.; Olsen, B.R.
 in: Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp.79-114, Academic Pre
 A;Title: The molecular biology of collagens with short triple-helical domains.
 A;Reference number: S22243
 A;Accession: S22243
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-674 <NIN>
 A;Cross-references: UNIPROT:P08125
 R;LuWalle, P.; Ninomiya, Y.; Rosenblum, N.D.; Olsen, B.R.
 A;Title: The type X collagen gene. Intron sequences split the 5'-untranslated region and
 A;Reference number: A31896; MUID:89054019; PMID:2461368
 A;Accession: A31896
 A;Molecule type: mRNA
 A;Residues: 1-75 <LUT>
 R;Ninomiya, Y.; Gordon, M.; van der Rest, M.; Schmid, T.; Linsenmayer, T.; Olsen, B.R.
 A;Cross-references: EMBL:MI13496; NID:9211699; PIDN:AAK48736.1; PID:9211700
 A;Accession: S77711
 A;Molecule type: protein
 A;Residue: I10-112; X; 114-117; 453-466 <NIN2>
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxyproline;
 P;1-18/Domain: signal sequence #status predicted <SIG>
 P;57-673/Domain: complement C1q carboxyl-terminal homology <C1Q>
 P;53; 456/Modified site: hydroxyproline (Pro) #status experimental
 P;611/Binding site: carbohydrate (Kan) (covalent) #status predicted
 Query Match 42.0%; Score 297.5; DB 2; Length 674;
 Best Local Similarity 47.6%; Pred. No. 6.8e-22;
 Matches 59; Conservative 21; Mismatches 43; Indels 1; Gaps 1;

Qy 1 PSVGLTYVTPNMPTRPKFYQDQHGDSTGKPHCNIPGLYPAHYITVIMKDVKVS 60
 Db 548 PTVLISKAYPKSATVPIKEDKLYRNQHYDRTGIFTCRIPGLYVFSYHFTAKGTVWVA 607
 Qy 61 IPKDKKMLFTYDQYQBNVVAQSGSVLHLFLEVGDQWLOVYGEGRNGLXADNDNSTF 120
 Db 608 LYKNGSPVWYTYDEOKGYLQDQASGSAVIDLMENDQWLOQ-PNSBSNGLYSEVWHSF 666
 Qy 121 TGFL 124
 Db 667 SGFL 670

RESULT 3
 CGHUND
 collagen alpha 1(X) chain precursor - human
 N;Alternate names: procollagen alpha 1(X) chain
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S26396; S30086; S15825; S18249; A43901; I51870; S21856
 R;Rechenberger, B.; Beier, F.; LuWalle, P.; Olsen, B.R.; von der Mark, K.; Bertling, W.
 A;Title: Genomic organization and full-length cDNA sequence of human collagen X.
 A;Accession: S26396; MUID:93012005; PMID:139733
 A;Molecule type: DNA
 A;Residues: 1-680 <REI>

A;Cross-references: UNIPROT:Q03592; EMBL:X8952; EMBL:X72578; EMBL:X72580; EMBL:X72579; EMBL:X72581
 R;Apte, S.S.
 A;Cross-references: EMBL:X65120; NID:931129
 A;Reference number: S30085
 A;Accession: S30085
 A;Molecule type: DNA
 A;Residues: 'TIPPGWGWVWLL', 52-600 <APT>
 A;Cross-references: EMBL:X65120; NID:931129
 A;Note: the initial difference is probably due to translation of an intronic sequence
 R;Apte, S.; Mattei, M.G.; Olsen, B.R.
 FEBS Lett. 282, 391-396, 1991
 A;Title: Cloning of human alpha-1(X) collagen DNA and localization of the COL10A1 gene t.
 A;Reference number: S15826; MUID:91243838; PMID:2037056
 A;Accession: S15826
 A;Molecule type: DNA
 A;Residues: 561-647, 'G', 649-666 <AP2>
 A;Cross-references: EMBL:X58979; NID:930013; PIDN:CAA41686.1; PID:930014
 R;Thomas, J.T.; Crosswell, C.J.; Rash, B.; Nicolai, H.; Solomon, E.; Grant, M.
 Biochem. J. 280, 617-623, 1991
 A;Title: The human collagen X gene. Complete primary translated sequence and chromosomal
 A;Reference number: S18249; MUID:92109659; PMID:1764025
 A;Accession: S18249
 A;Molecule type: DNA
 A;Residues: 1-26, 'T', 28-680 <TH0>
 A;Cross-references: EMBL:X63082; NID:930094; PIDN:CA42933.1; PID:930095
 A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 2 in having 532-Ala
 R;Reichenberger, E.; Aigner, T.; von der Mark, K.; Stoss, H.; Bertling, W.
 Dev. Biol. 149, 562-572, 1991
 A;Title: In situ hybridization studies on the expression of type X collagen in fetal hum
 A;Reference number: A43901; MUID:92077285; PMID:743401
 A;Accession: A43901
 A;Molecule type: mRNA
 A;Residues: 547-656 <RE2>
 A;Cross-references: GB:M74050; GB:D57494; NID:933984; PIDN:AA61221.1; PID:9553796
 A;Note: sequence extracted from NCBI backbone (NCBIN:69012, NCBI:69014)
 R;Wallis, G.A.; Rash, B.; Sweetman, W.A.; Thomas, J.T.; Super, M.; Evans, G.; Grant, M.B.
 Am. J. Hum. Genet. 54, 169-178, 1994
 A;Title: Amino acid substitutions of conserved residues in the carboxyl-terminal domain
 A;Comment: Proline and Lysines at the third position of the tripeptide repeating unit (ed and subsequently O-glycosylated).
 C;Genetics:
 A;Gene: GDB:COL10A1
 A;Cross-references: GDB:128635; OMIM:120110
 A;Map position: 6q1-6q22
 A;Introns: 52/1
 A;Note: a defect in this gene may cause Schmid metaphyseal chondroplasia
 C;Complex: type X collagen may be a homotrimer
 C;Function:
 A;Description: structural component of extracellular fibrous polymer specifically and tr
 be important for skeletogenesis
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer; hydroxylysine;
 P;1-18/Domain: signal sequence #status predicted <SIG>
 P;19-680/Domain: product: collagen alpha 1(X) chain #status predicted <MAT>
 P;19-56/Domain: amino-terminal nonhelical #status predicted <NC2>
 P;7-519/Domain: interrupted helical
 P;520-680/Domain: amino-terminal nonhelical #status predicted <NC1>
 P;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>
 P;617/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 40.6%; Score 287.5; DB 1; Length 680;
 Best Local Similarity 46.4%; Pred. No. 6.9e-21;
 Matches 58; Conservative 19; Mismatches 47; Indels 1; Gaps 1;

A;Molecule type: DNA
 A;Residues: 1-743 <MUR>
 A;Cross-references: UNIPROT:Q00780; EMBL:X66976; NID:950493; PIDN:CAA47387.1; PID:913599
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology <CIQ>
 F;616-742/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 38.6%; Score 273.5; DB 1; Length 743;
 Best Local Similarity 45.1%; Pred. No. 2e-19;
 Matches 55; Conservative 27; Mismatches 35; Indels 5; Gaps 2;
 QY 9 VTIPI---NMPIRFTKIFYQNYQHNGSTGKFKHCNTPGLYLYFAYHITVVMKDVKVLSLFKK 64
 Db 621 LIVPPPPVGAPVFKFDKLYNQKLYNQHNGSTGKFKHCNTPGLYLYFAYHITVVMKDVKVLSLFKK 64
 QY 65 DKAMKFLYTYDQYQENNYDQASGSVLLHLEVDQWLYQVYGERGLYADNDNDSTFTGFL 124
 Db 681 NEPMWMTYDEYKKGFLDQASGSVAVLLRPGDQFLQNPB-EQAGLYAQYVHSSFSGYL 739
 QY 125 LY 126
 Db 740 LY 741

RESULT 7
 S15335
 collagen alpha 1(VIII) chain precursor - human
 C;Species: Homo sapiens (man)
 C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C;Accession: S15435
 R;Muragaki, Y.; Mattei, M.G.; Yamaguchi, N.; Olsen, B.R.; Ninomiya, Y.
 Bur. J. Biochem. 197, 635-622, 1991
 A;Title: The complete primary structure of the human alpha-1(VIII) chain and assignment
 A;Reference number: S15435; MUID:91231001; PMID:2029894
 A;Accession: S15435
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-744 <MUR>
 A;Cross-references: UNIPROT:P27658; EMBL:X57527; NID:930081; PIDN:CAA40748.1; PID:930082
 C;Genetics:
 A;Gene: GDB:COIA81
 A;Cross-references: GDB:128104; OMIM:120251
 A;Map position: 3q11.1-3q13.2
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
 F;1-20/Domain: signal sequence #status predicted <SIG>
 F;21-744/Domain: collagen alpha 1(VIII) chain #status predicted <MAT>
 F;21-744/Region: amino-terminal nonhelical
 F;18-571/Region: interrupted helical
 F;572-743/Region: carboxyl-terminal nonhelical
 F;617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 37.8%; Score 267.5; DB 1; Length 744;
 Best Local Similarity 45.5%; Pred. No. 7.9e-19;
 Matches 51; Conservative 28; Mismatches 32; Indels 1; Gaps 1;
 QY 15 PIRFTKIFYQNYQHNGSTGKFKHCNTPGLYLYFAYHITVVMKDVKVLSLFKK 64
 Db 632 PIKFDRLLYNGRQNYDQGQFLGIFTCEVPGVYLYFAYHITVVMKDVKVLSLFKK 64
 QY 75 YQENNYDQASGSVLLHLEVDQWLYQVYGERGLYADNDNDSTFTGFLY 126
 Db 692 YKKGFLDQASGSVAVLLRPGDQFLQNPB-EQAGLYAQYVHSSFSGYL 742

RESULT 9
 S23298
 collagen alpha 1(VIII) chain - chicken
 C;Species: Gallus gallus (chicken)
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: S23298
 R;Ninomiya, Y.; Castagnola, P.; Gerecke, D.; Gordon, M.K.; Jacenko, O.; LuValle, P.; McC
 maguchi, N.; Olsen, B.R.
 in Extracellular Matrix Genes, Sandell L.J. and Boyd C.D., eds., pp. 79-114, Academic Pre
 A;Title: The molecular biology of collagens with short triple-helical domains.
 A;Reference number: S22243
 A;Accession: S23298
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-744 <NIN>
 A;Cross-references: UNIPROT:Q7LZR2
 C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology <CIQ>
 F;617-743/Domain: complement C1q carboxyl-terminal homology <CIQ>
 Query Match 37.2%; Score 263.5; DB 1; Length 744;
 Best Local Similarity 45.5%; Pred. No. 2e-18;
 Matches 51; Conservative 27; Mismatches 33; Indels 1; Gaps 1;
 QY 15 PIRFTKIFYQNYQHNGSTGKFKHCNTPGLYLYFAYHITVVMKDVKVLSLFKK 64
 Db 632 PIKFDRLLYNGRQNYDQGQFLGIFTCEVPGVYLYFAYHITVVMKDVKVLSLFKK 64
 QY 75 YQENNYDQASGSVLLHLEVDQWLYQVYGERGLYADNDNDSTFTGFLY 126
 Db 692 YKKGFLDQASGSVAVLLRPGDQFLQNPB-EQAGLYAQYVHSSFSGYL 742

RESULT 10
 B57131
 collagen alpha 2(VIII) chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004
 C;Accession: B57131
 R;Muragaki, Y.; Jaconko, O.; Apté, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.
 J. Biol. Chem. 266, 7721-7727, 1991
 A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen fami
 A;Reference number: A57131; MUID:9120292; PMID:2019595
 A;Accession: B57131
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-170 <MUR>
 A;Cross-references: UNIPROT:P25318; GB:M60833

RESULTS 8
 A34246
 collagen alpha 1(VIII) chain precursor - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Accession: A34246
 Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 R;Yamaguchi, N.; Benya, P.D.; van der Rest, M.; Ninomiya, Y.
 J. Biol. Chem. 264, 16022-16029, 1989
 A;Title: The cloning and sequencing of alpha1(VIII) collagen cDNAs demonstrate that type
 domains similar to those of type X collagen.

C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology

R;43-169/Domain: complement Clq carboxyl-terminal homology <Clq>

Query Match 36.5%; Score 258.5; DB 2; Length 170;

Best Local Similarity 40.8%; Pred. No. 1.1e-18; Mismatches 46; Indels 1; Gaps 1;

Matches 51; Conservative 27; MisMatches 46; Indels 1; Gaps 1;

A;Note: DKF2p5860621.1

Query Match 36.5%; Score 258.5; DB 2; Length 170;

Best Local Similarity 40.8%; Pred. No. 1.1e-18; Mismatches 46; Indels 1; Gaps 1;

Matches 51; Conservative 27; MisMatches 46; Indels 1; Gaps 1;

A;Note: DKF2p5860621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 65.0%; Score 510.5; DB 2; Length 219;

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 65.0%; Score 510.5; DB 2; Length 219;

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 65.0%; Score 510.5; DB 2; Length 219;

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

RESULT 11

A57131 collagen alpha 2(VIII) chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C;Accession: A57131

R;Murgaki, Y.; Jacekko, O.; Apte, S.; Mattei, M.G.; Ninomiya, Y.; Olsen, B.R.

J. Biol. Chem. 266, 7721-7727, 1991

A;Title: The alpha2(VIII) collagen gene. A novel member of the short chain collagen family

A;Reference number: A57131; MUID:91210292; PMID:2019595

A;Accession: A57131

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-635 <MUR>

A;Cross-references: UNIPROT:P25067; GB:MG0832; NID:917178; PIDN:AAA62822.1; PID:917179

C;Genetics: GDB:COLB2

A;Cross-references: GDB:127812; OMIM:120252

C;Map position: 1p34.3-1p2.3

C;Superfamily: collagen alpha 1(VIII) chain; complement Clq carboxyl-terminal homology

F;1-11/Domain: amino-terminal nonhelical (fragment) #status predicted <NC2>

P;12-468/Region: interdomain helical

P;469-635/Domain: carboxyl-terminal nonhelical #status predicted <NC7>

P;508-634/Domain: complement Clq carboxyl-terminal homology <Clq>

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

Query Match 36.5%; Score 258.5; DB 2; Length 635;

Best Local Similarity 40.0%; Pred. No. 5.2e-18; Mismatches 45; Indels 1; Gaps 1;

Matches 50; Conservative 29; MisMatches 45; Indels 1; Gaps 1;

RESULT 12

T14782 hypothetical protein DKPZp586B0621.1 - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004

C;Accession: T14782

R;Ottenwaelder, B.; Obermaier, B.; Mewes, H.W.; Gassner, J.; Wiemann, S.

submitted to the Protein Sequence Database, August 1999

A;Reference number: 218184

A;Accession: T14782

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-219 <OTT>

A;Cross-references: UNIPROT:Q9BXJ0; EMBL:All10261

A;Experiment: adult uterus; clone DKF2p586B0621

A;Genetics:

A;Note: DKF2p5860621.1

Query Match 34.4%; Score 243.5; DB 2; Length 219;

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 6 ETYVTP-NMPRTKIFQYDQHNPYDSTGKPHCNICLGLYFAYHTVYMKVSK 64

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 65 DKAMLIFTDQYQENNVA--SGSVLHLVLEGQDWLQLVYGEGERNLGKTYADNDNSTFG 122

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 65 GSS-LASFQFEGMPKPSLSGAMVRLPESDQWVQV-GYDYGIVYASITKTDSTFG 205

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 123 FLIYHD 128

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 206 FLVTS 211

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 CHIUC 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Query Match 313 C1Q 313

Best Local Similarity 42.4%; Pred. No. 4.7e-17; Mismatches 53; Indels 5; Gaps 4;

Matches 53; Conservative 23; MisMatches 45; Indels 5; Gaps 4;

A;Note: DKF2p5860621.1

Search completed: May 6, 2005, 17:30:49
Job time : 16.1497 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2005, 17:05:46 ; Search time 49.9028 Seconds

(without alignment(s))

1333.999 Million cell updates/sec

Title: US-10-072-159-11
Perfect score: 708
Sequence: 1 FSVGSLETYVTPNMPIRFTK..... YADNDNDSTPTGFLLYHDTN 130

Scoring table: BLOSUM62
Gapop 10.0 , Gapext: 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|-------|--------------------|----------|--------------------------|
| 1 | 708 | 100.0 | 244 | 1 APM1_HUMAN |
| 2 | 707 | 99.9 | 243 | 2 Q55QD7 |
| 3 | 661 | 93.4 | 2 Q8K3R4 | Q8K3R4 rattus norvegicus |
| 4 | 655 | 92.5 | 247 | 1 APM1_MOUSE |
| 5 | 655 | 92.5 | 247 | 2 Q8BHW2 |
| 6 | 633 | 89.4 | 244 | 2 Q76C76 |
| 7 | 615 | 86.9 | 240 | 2 Q95HQ4 |
| 8 | 594 | 83.9 | 242 | 2 Q6Q2K6 |
| 9 | 594 | 83.9 | 243 | 2 Q6PP07 |
| 10 | 586 | 82.8 | 243 | 2 Q7KRF8 |
| 11 | 557 | 78.7 | 244 | 2 Q6QH7 |
| 12 | 514 | 72.6 | 194 | 2 Q95I95 |
| 13 | 501 | 70.8 | 235 | 2 Q6D145 |
| 14 | 478 | 67.5 | 235 | 2 Q6GJS9 |
| 15 | 464 | 65.5 | 153 | 2 Q6JRS5 |
| 16 | 415 | 58.6 | 144 | 2 Q6V9B4 |
| 17 | 363 | 51.3 | 106 | 2 Q6Z226 |
| 18 | 355 | 50.2 | 333 | 2 Q8IT04 |
| 19 | 345 | 48.8 | 195 | 2 Q8BZS3 |
| 20 | 310 | 43.8 | 145 | 2 Q6VFT9 |
| 21 | 297 | 42.0 | 674 | 1 CALA_CHICK |
| 22 | 287 | 40.6 | 680 | 1 CALA_HUMAN |
| 23 | 286 | 40.4 | 419 | 1 COLE_LEPMA |
| 24 | 285 | 39.9 | 675 | 2 Q9N178 |
| 25 | 281 | 39.8 | 295 | 2 Q9Z1K4 |
| 26 | 281 | 39.7 | 508 | 1 OTOL_ONCKE |
| 27 | 280 | 39.6 | 674 | 1 CALA_BOVIN |
| 28 | 280 | 39.6 | 680 | 1 CALA_MOUSE |
| 29 | 280 | 39.6 | 743 | 1 CALA_MOUSE |
| 30 | 280 | 39.6 | 744 | 2 Q92188 |
| 31 | 280 | 39.6 | 744 | 2 Q8BGL6 |

| ALIGNMENTS | | | | |
|---|-----------|------|---------|--|
| RESULT 1 | | | | |
| ID APM1_HUMAN | STANDARD; | PRT; | 244 AA. | |
| AC Q15848; | | | | |
| DT 01-NOV-1997 (Rel. 35, Created) | | | | |
| DT 01-JAN-2005 (Rel. 46, Last annotation update) | | | | |
| DE Adiponectin precursor (Adipocyte, C1q and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30) | | | | |
| DE (Adipose most abundant gene transcript 1) (apm-1) (Gelatin-binding protein) | | | | |
| DE Name=ACRP30, APM1, GBP28; | | | | |
| GN Homo sapiens (Human). | | | | |
| OS Eukaryota; Metacozoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | | | | |
| OC NCBI_TaxID=9606; | | | | |
| OX RN [1] - | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RC TISSUE-Adipose tissue; | | | | |
| RA MEDLINE=96224171; PubMed=8619847; DOI=10.1006/bbrc.1996.0587; | | | | |
| RA Maeda K., Okubo K., Shimomura I., Funahashi T., Matsuzawa Y., Matsubara K., | | | | |
| RT "CDNA cloning and expression of a novel adipose specific collagen-like factor, apm1 (Adipose Most abundant Gene transcript 1)."; | | | | |
| RT Factor, apm1 (Adipose Most abundant Gene transcript 1)."; | | | | |
| RL Biochem. Biophys. Res. Commun. 221:286-289(1996). | | | | |
| RN [2] | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RA MEDLINE=99196984; PubMed=10095105; DOI=10.1016/S0378-1119(99)00041-4; | | | | |
| RA Saito K., Tobe T., Minoshawa S., Asakawa S., Sumiya J., Yoda M., Nakano Y., Shimizu N., Tomita M., | | | | |
| RA Nakano Y., Shimizu N., Tomita M., | | | | |
| RT "Organization of the gene for gelatin-binding protein (GBP28)."; | | | | |
| RL Gene 229:67-73(1999). | | | | |
| RN [3] | | | | |
| RP SEQUENCE FROM N.A. | | | | |
| RA MEDLINE=99333693; PubMed=10403784; DOI=10.1005/bbrc.1999.0865; | | | | |
| RA Schaeffler A., Orbo E., Palitzsch K.D., Buechner C., Dronik W., Fuerst A., Schoellmerich J., Schmitz G.; | | | | |
| RT "The human apm-1, an adipocyte-specific gene linked to the family of TNF's and to genes expressed in activated T cells, is mapped to chromosome 19q13-q23, a susceptibility locus identified for familial combined hyperlipidemia (FCH)."; | | | | |
| RT combined hyperlipidemia (FCH)."; | | | | |
| RL Biochem. Biophys. Res. Commun. 260:416-425(1999). | | | | |
| RN [4] | | | | |
| RP SEQUENCE OF 19-33. | | | | |
| RA PUBMED=15340161; DOI=10.1110/ps.04682504; | | | | |
| RA Zhang Z., Henzel W.J.; | | | | |
| RT "Signal peptide prediction based on analysis of experimentally verified cleavage sites.," | | | | |
| RT "Protein Sci. 13:2819-2824(2004)."; | | | | |
| RN [5] | | | | |
| RP SEQUENCE OF N-TERMINUS, AND PARTIAL SEQUENCE. | | | | |
| RA PUBMED=8941845; | | | | |
| RA Nakano Y., Tobe T., Choi-Miura N.H., Mazda T., Tomita M.; | | | | |
| RT "Isolation and characterization of GBP28, a novel gelatin-binding | | | | |

P27658 homo sapien
P14282 oryctolagus cuniculus
Q98Bu4 mus musculus
Q90xJ5 homo sapiens
Q8chx9 mus musculus
Q91xj2 homo sapiens
Q62789 sus scrofa
Q71rz2 gallus gallus
Q95mb2 equus caballus
P25318 mus musculus
Q6faq4 mus musculus
Q6P1c4 mus musculus
Q8Bvd7 mus musculus

RT protein purified from human plasma.";

CC J. Biochem. 120:803-812(1996),

CC [6]

CC R.P. CHARACTERIZATION.

CC RX MEDLINE=20417177; PubMed=10963870;

CC RA Ouchi N., Kihara S., Funahashi T., Tenner A.J., Tominaga Y.,

CC Matsuzawa Y.;

CC "Adiponectin, a new member of the family of soluble defense collagens, negatively regulates the growth of myelomonocytic progenitors and the functions of macrophages.";

CC RT Blood 96:1723-1732(2000).

CC RL [7]

CC R.P. CHARACTERIZATION.

CC RX MEDLINE=20440368; PubMed=10982546;

CC RA Ouchi N., Kihara S., Arita Y., Okamoto Y., Maeda K., Kuriyama H.,

CC RA Hotta K., Nishida M., Takahashi M., Muraguchi M., Ohmoto Y.,

CC RA Nakamatsu T., Yamashita S., Funahashi T., Matsuzawa Y.;

CC "Adiponectin, an adipocyte-derived plasma protein, inhibits endothelial NF- κ B signaling through a cAMP-dependent pathway.";

CC RT Circulation 102:1295-1301(2000).

CC RN [8]

CC R.P. FUNCTION.

CC RX MEDLINE=21372428; PubMed=11479627; DOI=10.1038/90984;

CC RA Yamauchi T., Kamon J., Waki H., Terauchi Y., Kubota N., Hara K.,

CC RA Mori Y., Ide T., Murakami K., Tsuboyama-Kasakawa N., Ezaki O.,

CC RA Akanuma Y., Gavrilova O., Vinson C., Reitman M.L., Keechikawa H.,

CC RA Shudo K., Yoda M., Nakano Y., Tobe K., Nagai R., Kimura S., Tomita M.,

CC RA Froguel P., Kadowaki T.;

CC "The fat-derived hormone adiponectin reverses insulin resistance associated with both lipatrophy and obesity.";

CC RT Nat. Med. 7:941-946(2001).

CC RN [9]

CC R.P. VARIANT ADIPONECTIN DEFICIENCY CYS-112.

CC RX MEDLINE=20378830; PubMed=10916532;

CC RA Takahashi M., Arita Y., Yamazaki K., Matsukawa Y., Okutomi K.,

CC RA Horie M., Shimomura I., Hotta K., Kuriyama H., Kihara S., Nakamura T.,

CC RA Yamashita S., Funahashi T., Matsuzawa Y.,

CC RT "Genomic structure and mutations in adipose-specific gene, adiponectin.";

CC RT Int. J. Obes. Relat. Metab. Disord. 24:861-868(2000).

CC RN [10]

CC R.P. VARIANTS ARG-84; MET-117; THR-164; SER-221 AND PRO-241.

CC RX MEDLINE=21671103; PubMed=11827266;

CC RA Hara K., Boutin P., Mori Y., Tobe K., Dina C., Yasuda K., Yamauchi T.,

CC RA Otabe S., Okada T., Eto K., Kadowaki H., Hagura R., Akanuma Y.,

CC RA Yasaki Y., Nagai R., Taniyama M., Matsubara K., Yoda M., Nakano Y.,

CC RA Kimura S., Tomita M., Kimura S., Ito C., Froguel P., Kadowaki T.;

CC RT "Genetic variation in the gene encoding adiponectin is associated with an increased risk of type 2 diabetes in the Japanese population.";

CC RT Diabetes 51:536-540(2002).

CC CC -1- FUNCTION: Important negative regulator in hematopoiesis and immune systems, may be involved in ending inflammatory responses through its inhibitory functions. Inhibits endothelial NF- κ B

CC CC signaling through a cAMP-dependent pathway. Inhibits TNF- α -induced expression of endothelial adhesion molecules. Involved in the control of fat metabolism and insulin sensitivity.

CC CC -1- SUBUNIT: Homooligomer (Potential).

CC CC -1- SUBCELLULAR LOCATION: Secreted.

CC CC -1- TISSUE SPECIFICITY: Synthesized exclusively by adipocytes and secreted into plasma.

CC CC -1- DISEASE/DEFECT: Defects in ACDC are the cause of adiponectin deficiency (MIM:054411). The result is a very low concentration of plasma adiponectin. Decreased adiponectin plasma levels are associated with obesity, insulin resistance, and diabetes type 2.

CC CC -1- PHARMACEUTICAL: Adiponectin might be used in the treatment of diabetes type 2 and insulin resistance.

CC CC -1- SIMILARITY: Contains 1 CIG domain.

CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

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CC DR EMBL; D45371; BAA02271; DR EMBL; AB012165; BAA86716.1; JOINED.

CC DR EMBL; AB012164; BAA86716.1; JOINED.

CC DR EMBL; AJ131460; CAB52413.1; JOINED.

CC DR PIR; JC4708; JC4708.

CC DR HSSP; Q60594; ICB28.

CC Genew; HGNC:13633; ACDC.

CC MIM; 605441; DR GO; GO:006091; P:energy pathways; TAS.

CC DR InterPro; IPR001073; CIG helix.

CC DR InterPro; IPR008161; CIG helix.

CC DR InterPro; IPR008160; Collagen.

CC DR InterPro; IPR008983; TNF_like.

CC DR Pfam; PF00386; CIG; 1.

CC DR Pfam; PF01391; Collagen; 1.

CC DR PRINTS; PR00007; COMPLEMENTC1Q.

CC DR ProDom; PD00007; CIG helix; 2.

CC DR PROSITE; PS50811; CIG; 1.

CC KW Collagen; Diabetes mellitus; Direct protein sequencing;

CC KW Disease mutation; Hormone; Hydroxylation; Obesity; Plasma;

CC KW Polymorphism; Repeat; Signal.

CC FT SIGNAL 1 18

CC FT CHAIN 19 24

CC FT DOMAIN 42 107

CC FT DISULFID 244

CC FT DOMAIN 108

CC FT DISULFID 36

CC FT MOD RES 44

CC FT MOD RES 47

CC FT MOD RES 53

CC FT MOD RES 62

CC FT MOD RES 71

CC FT MOD RES 76

CC FT MOD RES 86

CC FT MOD RES 95

CC FT MOD RES 104

CC FT CARBOHYD 230

CC FT VARIANT 84 84

CC FT VARIANT 112 112

CC FT VARIANT 117 117

CC FT VARIANT 164 164

CC FT VARIANT 221 221

CC FT VARIANT 241 241

CC FT SEQUENCE 244 AA; 26414 MW; 6486C1-204B1018 CRC64;

CC Query Match 100.0%; Score 708; DB 1; Length 244;

CC Best Local Similarity 100.0%; Pred. No. 5.1e-62;

CC Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC QY 1 FSVGLGTYVITPNMIRFTKPYQMQNHYNGSTGKFCNIPGLYFAYHATVWIKDVKIS 60

CC Db 115 FSVGLGTYVITPNMIRFTKPYQMQNHYNGSTGKFCNIPGLYFAYHATVWIKDVKIS 174

CC QY 61 LFKKKQKMLTYDQYQENNYDQASGSVVLHLEVDQWLVQYGERGRLYADNDNSRF 120

CC Db 175 LFKKKQKMLTYDQYQENNYDQASGSVVLHLEVDQWLVQYGERGRLYADNDNSRF 234

CC QY 121 TGFLLIHTDN 130

CC Db 235 TGFLIYHTDN 244

| | | | | |
|-----------------------|---|--|------|---------|
| RESULT 2 | Q95D77 | PRELIMINARY; | PRT; | 243 AA. |
| AC | Q95D77; | | | |
| DT | 01-DEC-2001 | (TREMBrel, 19, Created) | | |
| DT | 01-DEC-2001 | (TREMBrel, 19, Last sequence update) | | |
| DT | 01-OCT-2003 | (TREMBrel, 25, Last annotation update) | | |
| DE | Adiponectin. | | | |
| GN | Name=APM1; | | | |
| OS | Macaca mulatta (Rhesus macaque). | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae; | | | |
| OC | Cercopithecinæ; Macaca. | | | |
| OX | NCBI_TaxID=9514; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Adipose; | | | |
| RX | MEDLINE:21232234; PubMed=11334417; | | | |
| RA | Hotta K., Funahashi T., Bodkin N.L., Ortmeyer H.K., Arita Y., | | | |
| RA | Hanren B.C., Matsukawa Y.; | | | |
| RT | "Circulating concentrations of the adipocyte protein adiponectin are decreased in parallel with reduced insulin sensitivity during the progression to type 2 diabetes in rhesus monkeys." | | | |
| RT | Diaabetes 50:1126-1133 (2001). | | | |
| DR | EMBL: AP04407; AAC92202.1; -. | | | |
| DR | HSSE; Q60994; ICB8. | | | |
| DR | GO; GO:0006817; P:phosphate transport; IEA. | | | |
| DR | InterPro; IPR01073; Cld. | | | |
| DR | InterPro; IPR08161; Cldg. helix. | | | |
| DR | InterPro; IPR08160; Collagen. | | | |
| DR | Pfam; PF00386; Cldg. | | | |
| DR | Pfam; PF01391; Collagen; 1. | | | |
| DR | PRINTS; PR0007; COMPLEANC1Q. | | | |
| DR | PRODOM; PD00007; Cldg helix; 1. | | | |
| DR | SMART; SM00110; C1Q; 1. | | | |
| DR | PROSITE; PS01113; C1Q; 1. | | | |
| KW | Collagen. | | | |
| SQ | SEQUENCE. 243 AA; 26264 MW; 49445DAF2B4613FD CRC64; | | | |
| Query Match | 99 %; Score 707; DB 2; Length 243; | | | |
| Best Local Similarity | 99.2%; Pred. No. 6.4e-62; | | | |
| Matches | 129; Conservative 1; Mismatches 0; Indels 0; Gaps 0; | | | |
| QY | 1 FSVGLEYTVIPNMPIRFTKIFYNQONHICGOSTGKPHCNIPGLYFAVHITVMDVKVS 60 | | | |
| QY | 114 FSVGLEYTVIPNMPIRFTKIFYNQONHICGOSTGKPHCNIPGLYFAVHITVMDVKVS 173 | | | |
| Db | 61 LFKKKKAKMLFTYDQOENNYDQASGSVLLHLEVGQWQWQVYGERBERGLYADNDNSTF 120 | | | |
| Db | 174 LFKKKKAKMLFTYDQOENNYDQASGSVLLHLEVGQWQWQVYGERBERGLYADNDNSTF 233 | | | |
| QY | 121 TGFLLJHDTN 130 | | | |
| Db | 235 TGFLLJHDTN 244 | | | |
| RESULT 4 | | | | |
| APM1_MOUSE | | | | |
| ID | APM1_MOUSE STANDARD; | | | |
| AC | Q60994; Q62400; Q9C668; | | | |
| DT | 01-Nov-1997 (Rel. 35, Created) | | | |
| DT | 01-Nov-1997 (Rel. 35, Last sequence update) | | | |
| DT | 25-OCT-2004 (Rel. 45, Last annotation update) | | | |
| DB | Adiponectin precursor (Adipocyte, Cldg and collagen domain containing protein) (30 kDa adipocyte complement-related protein) (ACRP30) | | | |
| DB | (Adipocyte specific protein AdipoQ). | | | |
| DB | Name=Adcde; Synonyms=AcRp30, Adipog; Apml; | | | |
| OS | Mus musculus (Mouse); | | | |
| OC | Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. | | | |
| OX | NCBI_TaxID=10090; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=adipocyte; | | | |
| RX | MEDLINE:6607057; PubMed=7592907; DOI=10.1074/jbc.270.45.26746; | | | |
| RA | Scherer P.E., Williams S., Fogliano M., Baldini G., Iodish H.F.; | | | |
| RT | "A novel serum protein similar to C1Q, produced exclusively in adipocytes." | | | |
| RL | J. Biol. Chem. 270:26746-26749 (1995). | | | |
| RN | [2] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | TISSUE=Fibroblast; | | | |
| RX | MEDLINE:9620999; PubMed=8631877; DOI=10.1074/jbc.271.18.10697; | | | |
| RA | Hu E., Liang P., Spiegelman B.M.; | | | |
| RT | "AdipoQ is a novel adipose-specific gene dysregulated in obesity." | | | |
| RL | J. Biol. Chem. 271:10697-10703 (1996). | | | |
| RN | [3] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RX | Pubmed=1162643; DOI=10.1005/brc.2001.4217; | | | |
| RA | Das K., Lin Y., Widén E., Zhang Y., Scherer P.E.; | | | |
| RT | "Chromosomal localization, expression pattern, and promoter analysis of the mouse gene encoding adipocyte-specific secretory protein Acrp30." | | | |
| RT | Acta30.; | | | |

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TAXID=10090;
 RN [1]
 RP SBOQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein; PubMed=0349836; DOI=10.1016/S0076-6879(99)03004-9;
 RX RN Carninci, P.; Hayashizaki, Y.;
 RT "High-efficiency full-length cDNA cloning.";
 DR Meth. Enzymol. 303:19-44(1999).
 RN [2]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein; PubMed=1105660; DOI=10.1038/35055500;
 RA RIKEN PANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA The FANTOM Consortium' Exploration Research Group Phase I & II Team;
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 60,770 full-length cDNAs.";
 RL Nature 420:563-573 (2002).
 RN [4]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA MEDLINE=20049374; PubMed=11042159; DOI=10.1101/gr.145100;
 RA Carninci, P.; Shibata, Y.; Hayatsu, N.; Sugahara, Y.; Shibata, K.; Itoh, M.,
 RA Konno, H.; Ohazaki, Y.; Muramatsu, M.; Hayashizaki, Y.;
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1630(2000).
 RN [5]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA MEDLINE=20030913; PubMed=1107661; DOI=10.1101/gr.152600;
 RA Shibata, K.; Itoh, M.; Aizawa, K.; Nagaoka, S.; Sasaki, N.; Carninci, P.,
 RA Konno, H.; Akiyama, J.; Nishi, K.; Kitsunai, T.; Tashiro, H.; Itoh, M.,
 RA Sumi, N.; Iihoshi, Y.; Nakamura, S.; Hazama, M.; Nishine, T.; Harada, A.,
 RA Yamamoto, R.; Matsumoto, H.; Sakaguchi, S.; Ikegami, T.; Kashiwagi, K.,
 RA Fujiiwaka, S.; Inoue, K.; Togawa, Y.; Iiwa, M.; Ohara, E.; Watahiki, M.,
 RA Yoneda, Y.; Ishikawa, T.; Ochiai, T.; Tanaka, T.; Matsubara, S.; Kawai, J.,
 RA Okazaki, Y.; Muramatsu, M.; Inoue, Y.; Kita, A.; Hayashizaki, Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer.";
 DR Genome Res. 10:1757-1771(2000).
 RN [6]
 RP SSEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Aorta and vein;
 RA Adachi, J.; Aizawa, K.; Akimura, T.; Arikawa, T.; Bono, H.; Carninci, P.,
 RA Fukuda, S.; Furuno, M.; Hangaki, T.; Hara, A.; Hashizume, W.,
 RA Hayashida, K.; Hayatsu, N.; Hiramoto, K.; Hiraoka, T.; Hirozane, T.,
 RA Hori, F.; Imotani, K.; Ishii, Y.; Itoh, M.; Kagawa, I.; Kasukawa, T.,
 RA Katoch, H.; Kawai, J.; Kojima, Y.; Kondo, H.; Kouda, M.; Koya, S.,
 RA Kurihara, C.; Matsuyama, T.; Miyazaki, A.; Murata, M.; Nakamura, M.,
 RA Nishi, K.; Nomura, M.; Numazaki, R.; Ohno, M.; Ohnato, N.; Ohzaki, Y.,
 RA Saito, H.; Saitoh, H.; Sakai, C.; Sakai, N.; Sakaue, N.; Sano, H.,
 RA Sasaki, D.; Shibata, K.; Shinagawa, A.; Shiraki, T.; Sogabe, Y.; Tagami, M.,
 RA Tagawa, A.; Takahashi, F.; Takaku, Akahira, S.; Muramatsu, M.; Hayashizaki, Y.;
 RA Tomaru, A.; Toya, T.; Yabunishi, A.;
 DR Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK041994; BCAC30866.1; -.
 DR HSSP; Q60994; IC28.
 DR M6D; MGI; 10675; Adc.
 DR GO; GO:0005615; C: extracellular space; TAS.
 DR GO; GO:00105179; F: hormone activity; TAS.
 DR GO; GO:0010515; F: protein binding; IPI.
 DR GO; GO:0010635; F: fatty acid beta-oxidation; IMP.
 DR GO; GO:0006006; P: glucose metabolism; IDA.
 DR InterPro; IPR001073; Clq.

DR InterPro; IPR00161; Clg helix.
 DR InterPro; IPR00160; Collagen.
 DR InterPro; IPR00983; TNF_like.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen; 1.
 DR Pfam; PF00007; Clg helix; 1.
 DR SMART; SM00110; Clq; 1.
 DR PROSITE; PS01113; Clq; 1.
 DR Collagen.
 SQ SSEQUENCE 247 AA; 26751 MW; 0D3FF64C789CAEF3 CRC64;

DR Query Match 92.5%; Score 655; DB 2; Length 247;
 DR Best Local Similarity 91.5%; Pred. No. 9; 3e-5%; Indels 0; Gaps 0;
 DR Matches 119; 7; Mismatches 4; Indels 0; Gaps 0;

QY 1 FSVGLETVTTINMPFIFTKIRYQHNGDSTGKFRHICNIPGLYVYAHITYTMKVRS 60
 DR Db 118 FSVGLERTRVTVNVPKPFIFTKIRYQHNGDSTGKFRHICNIPGLYVYAHITYTMKVRS 177
 DR Qy 61 LFVKDKMLFTYDQYQNNVQASGTYLHSVGVQWLYQVGEGBRGLYADNDNISTF 120
 DR Db 178 LFVKDKMLFTYDQYQNNVQASGTYLHSVGVQWLYQVGEGBRGLYADNDNISTF 237
 DR Qy 121 TGFLLYDTN 130
 DR Db 238 TGFLLYDTN 247

DR RESULT 6
 DR Q76C76
 DR Q76C75 PRELIMINARY; PRT; 244 AA.
 DR AC 076C75;
 DR DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DR DT 05-JUN-2004 (Tremblrel. 27, Last annotation update)
 DR DE Adiponectin.
 DR Name=ppML;
 DR Canis familiaris (Dog).
 DR OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DR OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 DR RN [1] NCBI_TAXID=9615;
 DR RP SSEQUENCE FROM N.A.
 DR RA Ishioka, K.; Omachi, A.; Sagawa, M.; Shibata, H.; Honjoh, T.; Kimura, K.,
 DR RA Saito, M.; Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB10099; BAD15362.1;
 DR GO; GO:0005737; C:cytoplasm; IBA.
 DR GO; GO:000817; P:phosphate transport; IBA.
 DR InterPro; IPR001073; Clq.
 DR InterPro; IPR00160; Collagen.
 DR InterPro; IPR00160; Collagen.
 DR InterPro; IPR008161; Clg helix.
 DR InterPro; IPR00160; Collagen.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen; 1.
 DR PROSITE; PS00007; COMPLEMNC1Q.
 DR PRODOM; PD00007; Clg helix; 1.
 DR SMART; SM00110; Clq; 1.
 DR PROSITE; PS01113; Clq; 1.
 DR Collagen.
 SQ SSEQUENCE 244 AA; 26361 MW; 58659B7CC8865FB8 CRC64;

DR Query Match 89.4%; Score 633; DB 2; Length 244;
 DR Best Local Similarity 86.9%; Pred. No. 1; 4e-54%; Indels 0; Gaps 0;
 DR Matches 113; 11; Mismatches 6; Indels 0; Gaps 0;

QY 1 FSVGLETVTTINMPFIFTKIRYQHNGDSTGKFRHICNIPGLYVYAHITYTMKVRS 60
 DR Db 115 FSVGLERTRVTVNVPKPFIFTKIRYQHNGDSTGKFRHICNIPGLYVYAHITYTMKVRS 174
 DR Qy 61 LFVKDKMLFTYDQYQNNVQASGTYLHSVGVQWLYQVGEGBRGLYADNDNISTF 120

| | | | | | |
|-----------------------|---|--|-----------|---|-----|
| QY | 121 | TGFLILYHDTN | 130 | LYKKDKAMLFVYDQYQEKKNDQASGSVILHLEVGQWILQVY-CGDSVKGIVAYDNVNDSTF | 234 |
| Db | 235 | TGFLILYHDTN | 244 | | |
| | | | | | |
| RESULT 7 | | | | | |
| Q95MQ4 | | PRELIMINARY; | PRT; | 240 AA. | |
| ID | Q95MQ4 | | | | |
| AC | Q95MQ4; | | | | |
| DT | 01-DEC-2001 | (TREMBlrel. 19, Created) | | | |
| DT | 01-DEC-2001 | (TREMBl. 19, Last sequence update) | | | |
| DT | 01-OCT-2003 | (TREMBlrel. 25, Last annotation update) | | | |
| DB | | Adipose tissue-specific protein adipo Q. | | | |
| OS | Bos taurus (Bovine) | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos | | | | |
| OC | NCBI_TaxID:9913; | | | | |
| RN | | | | | |
| RP | | SEQUENCE FROM N.A. | | | |
| RX | | Medline:21369933; PubMed:11382781; DOI:10.1074/jbc.M104148200; | | | |
| RA | Sato, C.; Yasuhara, Z.; Honda, N.; Matsuda, T.; Kitajima, K.; | | | | |
| RT | "Identification and adipocyte differentiation-dependent expression of the unique diisialic acid residue in an adipose tissue-specific glycoprotein, adipo Q," | | | | |
| RT | J. Biol. Chem. 276:28849-28856 (2001). | | | | |
| RL | EMBL; AR269230; ARK58902.1; -. | | | | |
| DR | GO; GO:005737; C:cytoplasm; IEA. | | | | |
| DR | GO; GO:0006817; P:phosphate transport; IEA. | | | | |
| DR | InterPro; IPR01073; CIG. | | | | |
| DR | InterPro; IPR08160; Collagen. | | | | |
| DR | PF00386; CIG; 1. | | | | |
| DR | PFam; PF01391; Collagen; 1. | | | | |
| DR | PRINTS; PR00007; CIG helix; 2. | | | | |
| DR | ProDom; PDD00007; CIG helix; 2. | | | | |
| DR | SMART; SM00110; C10; 1. | | | | |
| DR | PROSITE; PS01113; CIG; 1. | | | | |
| DR | Collagen. | | | | |
| FT | NON_TER | | | | |
| SQ | SEQUENCE | 242 AA: | 26265 MW: | 1F3284A902E87D6D CRC64; | |
| Query Match | 83.9% | Score 594; DB 2; Length 242; | | | |
| Best Local Similarity | 83.6% | Pred. No. 1e-50; Mismatches 9; Indels 0; Gaps 0; | | | |
| Matches | 107; | Conservative | | | |
| QY | 1 | FSVGLETTYVTPNMPIRETKIFVNQHGDGTSKFKHONIPGKLYFAHITYMVDKVS | 60 | | |
| Db | 113 | FSVGLETRYVTPNMPIRETKIFVNQHGDGTSKFKHONIPGKLYFAHITYMVDKVS | 172 | | |
| QY | 61 | LFKKDKAMLFVYDQYQENNDQASGSVILHLEVGQWILQVY-GERBENGLYNDNDSTF | 120 | | |
| Db | 173 | LYKKDKAVLFVYDQYQENNDQASGSVILHLEVGQWILQVY-GERBENGLYNDNDSTF | 232 | | |
| QY | 121 | TGFLILYHD 128 | | | |
| Db | 233 | TGFLILYH 240 | | | |
| RESULT 8 | | | | | |
| Q6P07 | | PRELIMINARY; | PRT; | 243 AA. | |
| ID | Q6P07 | | | | |
| AC | Q6P07; | | | | |
| DT | 05-JUL-2004 | (TREMBl. 27, Created) | | | |
| DT | 05-JUL-2004 | (TREMBlrel. 27, Last sequence update) | | | |
| DE | Adiponectin. | | | | |
| OS | Sus scrofa (pig). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suis; Suidae; Sus. | | | | |
| OC | NCBI_TaxID:9823; | | | | |
| RN | | | | | |
| RP | | SEQUENCE FROM N.A. | | | |
| RA | Chowdhury, C.J.; Liu, B.H.; Ding, S.T.; | | | | |
| RL | Submitted (APR-2004) to the EMBL/GenBank/DBJ databases. | | | | |
| DR | EMBL; AR589691; AR00459.1; -. | | | | |
| DR | GO; GO:005737; C:cytoplasm; IEA. | | | | |
| DR | GO; GO:0006817; P:phosphate transport; IEA. | | | | |
| DR | InterPro; IPR01073; CIG. | | | | |
| DR | InterPro; IPR08161; CIG helix. | | | | |
| DR | InterPro; IPR08160; Collagen. | | | | |
| DR | InterPro; IPR00893; TNF like. | | | | |
| DR | PFam; PF00386; CIG; 1. | | | | |
| DR | PFam; PF01391; Collagen; 1. | | | | |
| DR | PRINTS; PR00007; CIG helix; 2. | | | | |
| DR | SMART; SM00110; C10; 1. | | | | |
| DR | Collagen. | | | | |
| SQ | SEQUENCE | 243 AA: | 26370 MW: | B886026A3C7C4474 CRC64; | |
| Query Match | 83.9% | Score 594; DB 2; Length 243; | | | |
| Best Local Similarity | 83.6% | Pred. No. 1e-50; | | | |

DR PROSITE; PS0113; C1Q; 1.
 KW Collagen.
 KW Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
 FT NON-TER 1 1
 FT NON-TER 194 194 MW; 3AA3D947D187AF9A CRC64;
 SQ SEQUENCE 194 AA; 20890 MW; 3AA3D947D187AF9A CRC64;
 Query Match 72.6%; Score 514; DB 2; Length 194;
 Best Local Similarity 89.3%; Pred. No. 6.8e-43; Length 235;
 Matches 92; Conservative 8; Mismatches 3; Indels 0; Gaps 0;
 AC 06D45; PRELIMINARY; PRT; 235 AA.
 DT 25-OCT-2004 (TREMBrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBrel. 28, Last annotation update)
 DE Col1al-prov protein.
 GN Name=col1al-prov;
 OS Xenopus tropicalis (Western clawed frog) (*Silurana tropicalis*).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=whole body;
 RA Klein S., Gerhard D.S.;
 RA InterPro; IPR008160; Collagen.
 DR InterPro; IPR008983; TNF-like.
 DR Pfam; PF00386; C1Q; 1.
 DR Pfam; PF01391; Collagen; 1.
 DR PRINTS; PR0007; COMPLEMTC1Q.
 DR SMART; SM00110; C1Q; 1.
 DR PROSITE; PS0113; C1Q; 1.

DR PROSITE; PS0113; C1Q; 1.
 KW Collagen.
 KW Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
 FT NON-TER 1 1
 FT NON-TER 194 194 MW; 558275AA3C872A32 CRC64;
 SQ SEQUENCE 194 AA; 25562 MW; 558275AA3C872A32 CRC64;
 Query Match 70.8%; Score 501; DB 2; Length 235;
 Best Local Similarity 68.8%; Pred. No. 1.6e-41; Length 20;
 Matches 88; Conservative 20; Mismatches 20; Indels 0; Gaps 0;
 AC 06G1S9; PRELIMINARY; PRT; 235 AA.
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DE MGC4292 protein.
 GN Name=MGC4292;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae; Xenopus.
 RN NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McEwan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalius D.E., Schnech A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RT Dev. Dyn. 225:384-391 (2002).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Klein S., Gerhard D.S.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBBJ databases.
 EMBL; BC074375; AAH74375.1; -.

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